

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 20:24:38 ; Search time 88 Seconds
(without alignments)
1372.371 Million cell updates/sec

Title: US-09-703-951A-8
Perfect score: 2456
Sequence: 1 MAARGSPRALRLLLVQLV.....PVIYKWNILIPVHIGNANK 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 23.*

1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_todent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2248	91.5	475	Q8SPU7	Q8spu7 bos taurus
2	2085.5	84.9	432	11 Q9QXK6	Q9qxk6 mus musculus
3	1623.5	56.1	363	11 Q8BIE9	Q8bie9 mus musculus
4	1572.5	64.0	462	13 Q8AV68	Q8av68 brachydanio
5	1526	62.1	464	11 Q8R5H3	Q8r5h3 mus musculus
6	1526	62.1	464	11 Q8BWN3	Q8bwn3 mus musculus
7	1427.5	58.1	449	11 Q9CVK8	Q9cvk8 mus musculus
8	1186.5	48.3	512	11 Q91X60	Q91x60 mus musculus
9	1153.5	47.0	629	11 Q9ET51	Q9et51 mus musculus
10	1147	46.7	494	11 Q8KOA7	Q8koa7 mus musculus
11	1144.5	46.6	629	11 Q8BHE9	Q8bhe9 mus musculus
12	1139	46.4	494	11 Q9ROW9	Q9row9 mus musculus
13	1097.5	44.7	499	11 Q8VHH6	Q8vhh6 mus musculus
14	1097.5	44.7	499	11 Q8R4G9	Q8r4g9 mus musculus
15	1097.5	44.7	504	11 Q8BV44	Q8bv44 mus musculus
16	1075.5	43.8	536	5 Q8T0Y9	Q8t0y9 alysia cal

17	1074.5	43.8	536	5 Q8T9S0	Q8t9s0 alysia cal
18	1065.5	43.4	515	5 Q46133	Q46133 locusta mig
19	1064.5	43.3	537	5 Q8MUR0	Q8mur0 apis mellif
20	1062.5	43.3	523	5 Q46128	Q46128 heliothis v
21	1051	42.8	531	5 Q96632	Q96632 heliothis v
22	1045.5	42.6	502	5 Q9NS87	Q9ns87 caenorhabdi
23	1039	42.3	533	5 Q8WRS1	Q8wrs1 chilo suppr
24	1025.5	41.8	567	5 Q9VC74	Q9vc74 drosophila
25	1024.5	41.7	537	5 Q9U941	Q9u941 myzus persi
26	1015	41.3	495	11 Q8R493	Q8r493 mus musculu
27	1009.5	41.1	489	4 Q9BR84	Q9br84 homo sapien
28	1004	40.9	457	6 Q9XS62	Q9xs62 canis famli
29	1002.5	40.8	532	5 Q9U940	Q9u940 myzus persi
30	1002	40.8	496	6 Q8SPU6	Q8spu6 bos taurus
31	995.5	40.5	532	5 Q8MUB6	Q8mub6 aphid gossy
32	989	40.3	545	5 Q96631	Q96631 heliothis v
33	980	39.9	501	11 Q9ERK7	Q9erk7 mus musculu
34	980	39.9	501	11 Q9R291	Q9r291 mus musculu
35	980	39.9	501	11 Q8BGP7	Q8bgp7 mus musculu
36	979.5	39.9	568	5 Q9NFR5	Q9nfr5 drosophila
37	970.5	39.5	540	5 Q46134	Q46134 locusta mig
38	964.5	39.3	341	11 Q8V111	Q8v111 mus musculu
39	962.5	39.2	595	5 P91764	P91764 myzus persi
40	962	39.2	500	11 Q9ROC3	Q9roc3 mus musculu
41	935.5	38.1	559	5 Q46132	Q46132 locusta mig
42	929	37.8	552	5 P91765	P91765 myzus persi
43	918.5	37.4	497	5 Q46135	Q46135 locusta mig
44	918.5	37.4	509	5 Q9NFX8	Q9nfx8 myzus persi
45	915.5	37.3	795	5 Q18394	Q18394 drosophila

ALIGNMENTS

RESULT 1

Q8SPU7	ID	Q8SPU7	PRELIMINARY;	PRT;	475 AA.
AC	Q8SPU7;				
DT	01-JUN-2002	(TrEMBLrel. 21, Created)			
DT	01-JUN-2002	(TrEMBLrel. 21, Last sequence update)			
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)			
DE	Neuronal nicotinic acetylcholine receptor alpha5 subunit.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97156643; PubMed=9003033;				
RA	Campos-Caro A., Smillie F.I., Dominguez del Toro E., Rovira J.C.,				
RA	Vicente-Agullo F., Chapuli J., Juiz J.M., Sala S., Sala F.,				
RA	Ballesta J.J., Criado M.;				
RT	"Neuronal nicotinic acetylcholine receptors on bovine chromaffin				
RT	cells: cloning, expression, and genomic organization of receptor				
RT	subunits."				
RL	J. Neurochem. 68:488-497(1997).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Campos-Caro A., Criado M.;				
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.				
DR	EMBL; AF187464; AAL8711.1;				
DR	InterPro; IPR006201; Neur channel.				
DR	InterPro; IPR006202; Neur chan LBD.				
DR	InterPro; IPR006029; Neu Channel memb.				
DR	Pfam; PF02931; Neur chan LBD; 1				
DR	Pfam; PF02932; Neur chan memb; 1				
DR	TIGRfam; TIGR00860; LIC; 1.				
DR	PROSITE; PS00236; NEUROTR ION CHANNEL; 1.				
KW	Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;				
KW	Transmembrane.				

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SQ SEQUENCE 475 AA; 54259 MW; 24658023DF0E3D1A CRC64;
Query Match 84.9%; Score 2085.5; DB 11; Length 432;
Best Local Similarity 90.1%; Pred. No. 2.1e-166;
Matches 390; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

QY 5 GSGPRAURLLLLVOLVAGRCGLAGAGAGRGISEPSSIAKHEDSLKDLFQDYERWVRP 64
Db 12 GLGFLQLQVLPQLVAGRWGPEGAGGVRGLAEPVSAKHEDSLFQDYERWVRP 71
QY 65 VEHLNDKIKFKGLAISQVLDVDEKQNMNTNWLKQEWIDVLRWNPDDYGGIKVIRP 124
Db 72 VEHLNDKIKFKGLAISQVLDVDEKQNMNTNWLKQEWIDVLRWNPDDYGGIKVIRP 131
QY 125 SDSVWTPDVLFDNADGRFGSTKTVIRYNGVTWTPPNYKSSCTIDVTFPPFDLQNC 184
Db 132 SDSLWTPDVLFDNADGRFGSTKTVIRYNGVTWTPPNYKSSCTIDVTFPPFDLQNC 191
QY 185 SMKFGSWTYDGSQVDIILEDDQDVKRDFDNGEWEIVSATGSKGNRTDSCWYPYTYSF 244
Db 192 SMKFGSWTYDGSQVDIILEDDQDVKRDFDNGEWEIVSATGSKGNRTDSCWYPYTYSF 251
QY 245 VIKRLPLFYFLFIIPICIGISFLTVLYPLSPNEGEKICLCTSVLSLTVFLVIEEIIIP 304
Db 252 VIKRLPLFYFLFIIPICIGISFLTVLYPLSPNEGEKICLCTSVLSLTVFLVIEEIIIP 311
QY 305 SSSKVIPLICEYLVTMIFVTLTSMVTVFVAINIHRSSSTHNAMAPLVKIFLHTLPKLL 364
Db 312 SSSKVIPLICEYLVTMIFVTLTSMVTVFVAINIHRSSSTHNAMAPLVKIFLHTLPKLL 371
QY 365 CMRSHVDYRFTQKEETSGSGPKSSRNTLEAALNSIRYIIRHMKENDVREVEDWKFFIA 424
Db 372 CMRSHVDYRFTQKEETSGSGPKSSRNTLEAALNSIRYIIRHMKENDVREVEDWKFFIA 431
QY 425 QVLDRLMFLTWFLFVSVISGLFVPVIYKXANLIPVHIGNANK 468
Db 432 QVLDRLMFLTWFLFVSVISGLFVPVIYKXANLIPVHIGNANK 475

RESULT 2
Q9QXK6 PRELIMINARY; PRT; 432 AA.
AC Q9QXK6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 5 subunit (Fragment).
GN ACR45.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/21bg; TISSUE=Interpeduncular nucleus of brain;
RA Stitzel J.A., Blanchette J.M.;
RT "Cloning of mouse nicotinic receptor alpha 5 subunit cDNA.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF204689; AFI9423.1; -.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
FT NON_TER
SQ SEQUENCE 432 AA; 49635 MW; 640881B448C4FD4C CRC64;

Query Match 66.1%; Score 1623.5; DB 11; Length 363;
Best Local Similarity 68.8%; Pred. No. 9e-128;
Matches 322; Conservative 17; Mismatches 24; Indels 105; Gaps 2;

QY 1 MAARGSPRALRLILLVQLVAGRCGLAGAGAGRGISEPSSIAKHEDSLKDLFQDYER 60
Db 1 MAARGSPRALRLILLVQLVAGRCGLAGAGAGRGISEPSSIAKHEDSLKDLFQDYER 60
QY 61 WVRPVEHLNDKIKFKGLAISQVLDVDEKQNMNTNWLKQEWIDVLRWNPDDYGGIKV 120
Db 35 ----- 34

RESULT 3
Q8BIE9 PRELIMINARY; PRT; 363 AA.
AC Q8BIE9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE NICOTINIC receptor alpha 5 subunit homolog.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/60; TISSUE=Adipose tissue;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK080900; BAC38070.1; -.
SQ SEQUENCE 363 AA; 41327 MW; BFC17A2AE1146DC1 CRC64;

Query Match 66.1%; Score 1623.5; DB 11; Length 363;
Best Local Similarity 68.8%; Pred. No. 9e-128;
Matches 322; Conservative 17; Mismatches 24; Indels 105; Gaps 2;

QY 1 MAARGSPRALRLILLVQLVAGRCGLAGAGAGRGISEPSSIAKHEDSLKDLFQDYER 60
Db 1 MAARGSPRALRLILLVQLVAGRCGLAGAGAGRGISEPSSIAKHEDSLKDLFQDYER 60
QY 61 WVRPVEHLNDKIKFKGLAISQVLDVDEKQNMNTNWLKQEWIDVLRWNPDDYGGIKV 120
Db 35 ----- 34
```

QY 121 IRVPSDVTDPDVLVDNADGRFEGTSTKTVIRYNGTWTWTPPANKYSSCTIDVTFPPD 180
DB 35 -----GDGRFEGASTKTIVRYNGTWTWTPPANKYSSCTIDVTFPPD 76
QY 181 LONCSMKFGSWYDGSQVDIILEDQDVDRDFDNGEWEIFVSATGSKGNRTDSCCWPYV 240
DB 77 LONCSMKFGSWYDGSQVDIILEDQDVDRDFDNGEWEIFVSATGSKGNRTDSCCWPYV 136
QY 241 TYSFVKRLPLFLFTLLIIPICIGLSPLTVLVFVLPNSGEKICLCTSVLSVLTFLVIE 300
DB 137 TYSFVKRLPLFLFTLLIIPICIGLSPLTVLVFVLPNSGEKICLCTSVLSVLTFLVIE 196
QY 301 EIIPSSKVIPLIGEVLVTMIFVLTSLIMVTVPAINIHRSSSTHNAAPLVKIFLHTL 360
DB 197 EIIPSSKVIPLIGEVLVTMIFVLTSLIMVTVPAINIHRSSSTHNAAPLVKIFLHTL 256
QY 361 PKLLCNRSHVDYFYQKEETESGPKSSRNTLEALNSIRYTRHMKENDVREVEDW 420
DB 257 PKLLCNRSHVDYFYQKEETESGPKSSRNTLEALNSIRYTRHMKENDVREVEDW 315
QY 421 KFAIQVLDNFMFLWTFVLSVIGSLGFVPIVKWANIILIPVHIGNANK 468
DB 316 KFAIQVLDNFMFLWTFVLSVIGSLGFVPIVKWANIILIPVHIGNANK 363

RESULT 4

Q8AV68 PRELIMINARY; PRT; 462 AA.
ID Q8AV68
AC Q8AV68
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor beta3 subunit.
GN NACHR-BETA3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22338858; PubMed=12451132;
RA Tokunaka H., Yoshida T., Matsuda N., Mishina M.;
RT "Regulation by Glycogen Synthase Kinase-3beta of the Arborization
Field and Maturation of Retinorectal Projection in Zebrafish."
RL J. Neurosci. 22:10324-10332(2002).
DR EMBL; AB087185; BAC41198.1; -.
KW Receptor.
SQ SEQUENCE 462 AA; 53197 MW; 9F396990DBA30964 CRC64;

Query Match 64.0%; Score 1572.5; DB 13; Length 462;
Best Local Similarity 67.8%; Pred. No. 2.3e-123;
Matches 288; Conservative 63; Mismatches 59; Indels 15; Gaps 3;
QY 42 STAKHEDSLKDLFDYERWRVPEHLNDKIKIFGLAISQVLDVDEKQNLMTNVLKQ 101
DB 26 SLAEREDALLRLDFQYQWRVPEHLNDKIKIFGLAISQVLDVDEKQNLMTNVLKQ 85
QY 102 EMDVLRNPDYGGIKVIRVPSDVTDPDVLVDNADGRFEGT-STKTVIRYNGTWTW 160
DB 86 EMDVLRNPDYGGIKVIRVPSDVTDPDVLVDNADGRFEGT-STKTVIRYNGTWTW 145
QY 161 TTPANKYSSCTIDVTFPPDLONCSMKFGSWYDGSQVDIILEDQDVDRDFDNGEWEIF 220
DB 146 TTPANKYSSCTIDVTFPPDLONCSMKFGSWYDGSQVDIILEDQDVDRDFDNGEWEIF 205
QY 221 VBATGSKGNRTDSCCWPYVYTSFVKRLPLFLFTLLIIPICIGLSPLTVLVFVLPNSGE 280
DB 206 VBATGSKGNRTDSCCWPYVYTSFVKRLPLFLFTLLIIPICIGLSPLTVLVFVLPNSGE 265
QY 281 KICLCTSVLSVLTFLVLTVEEIIIPSSSKVIPLIGEVLVTMIFVLTSLIMVTVPAINIHR 340

DB 266 KVSLSVLSVLTFLVLTVEEIIIPSSSKVIPLIGEVLVTMIFVLTSLIMVTVPAINIHR 325
QY 341 SSSTHNAAPLVKIFLHTLPLKLCMRSHVDYFYQKEETESGPKSSR----- 390
DB 326 SSATVHPSPWVRLTFLQRLPDLCCMRGNTDRYHYVQMPQSPDLKPKSKGPPGEGDG 385
QY 391 -----NTLEAALNSIRYTRHMKENDVREVEDWKFIAQVLDNFMFLWTFVLSVIGSL 446
DB 386 QALINMLEQATNSVRYISRHKKHFIREVVDWKFVQAQVLDRIFLWAFLTVSVLGTILI 445
QY 447 FVPIV 451
DB 446 FVPAV 450

RESULT 5

Q8R5H3 PRELIMINARY; PRT; 464 AA.
ID Q8R5H3
AC Q8R5H3
DT 01-JUN-2002 (TremBLrel. 21, Created)
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor beta 3 subunit.
GN CHRN3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Stitzel J.A., Lautner M.A., Jimenez M., Bhandarkar S.J., Curtis C.D.,
RA Remias J.;
RT "Isolation of a mouse nicotinic acetylcholine receptor Beta 3 subunit
cDNA."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF467896; AAL75573.1; -.
DR InterPro; IPR006201; Neur channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 464 AA; 53140 MW; 823AB7B250D72034 CRC64;

Query Match 62.1%; Score 1526; DB 11; Length 464;
Best Local Similarity 65.8%; Pred. No. 1.8e-119;
Matches 289; Conservative 66; Mismatches 64; Indels 20; Gaps 4;
QY 33 AORGLSEPSSTAKHEDSLKDLFDYERWRVPEHLNDKIKIFGLAISQVLDVDEKQNL 92
DB 24 ATAGL-----SSVAHEDEALLRLDFQYQWRVPEHLNDKIKIFGLAISQVLDVDEKQNL 80
QY 93 MTTNVLKQEWIDVLRNPDYGGIKVIRVPSDVTDPDVLVDNADGRFEGT-STKTV 151
DB 81 MTTNVLKQEWIDVLRNPDYGGIKVIRVPSDVTDPDVLVDNADGRFEGT-STKTV 140
QY 152 IRYNGTWTWTPPANKYSSCTIDVTFPPDLONCSMKFGSWYDGSQVDIILEDQDVDRD 211
DB 141 VKSSGTWSTWTPASYKSSCTMDVTFPPDLONCSMKFGSWYDGSQVDIILEDQDVDRD 200
QY 212 PFDNGEWEIFVSATGSKGNRTDSCCWPYVYTSFVKRLPLFLFTLLIIPICIGLSPLTVLV 271
DB 201 PFDNGEWEIFVSATGSKGNRTDSCCWPYVYTSFVKRLPLFLFTLLIIPICIGLSPLTVLV 260
QY 272 PFLSNRGEKICLCTSVLSVLTVEEIIIPSSSKVIPLIGEVLVTMIFVLTSLIMVT 331
DB 261 PFLSNRGEKICLCTSVLSVLTVEEIIIPSSSKVIPLIGEVLVTMIFVLTSLIMVT 320

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QY 332 VFAINIHRSSSTHNAAPLVKIFLHTLPKLLCMRSHVDYF-----TQKEETESGGPK 387
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 321 VFVINVHRSSSTVHPNAPVWKLFLEKLPWLCKDPRDRFSPDGTESKGVGRGKFP 380

QY 388 SSRNT-----LEAALNSIRYITRHKENDVREVEDKFIQVLDRLMFWTF 435
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 381 KKGQTPTSDGERVLVAFLEKASESIRYISRVKKEHFISQVQDKFVAQVLDRIFLWLF 440
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 436 LFVSIIVGSLGLFVPVIYKW 454
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 441 LTASVLGSLVLIIFPALQKW 459

RESULT 6
Q8BMN3 PRELIMINARY; PRT; 464 AA.
AC Q8BMN3 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Neuronal acetylcholine receptor protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK030464; BAC26973.1; -.
SQ SEQUENCE 464 AA; 53112 MW; 2CEA3E0DAF2D5EB CRC64;

Query Match 62.1%; Score 1526; DB 11; Length 464;
Best Local Similarity 65.8%; Pred. No. 1.8e-119;
Matches 289; Conservative 66; Mismatches 64; Indels 20; Gaps 4;
```

```
QY 33 AORGLSEPSIAKHEDSLKDLFQDYERWVRVPEHLNDKIKIFGLAISQLVDVDEKNQL 92
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 24 ATAGL-----SSVAEHEDALLRHFLFGYQKCVRPVLNSSDIIKVFGLKISQLVDVDEKNQL 80

QY 93 MTTNWLKQEWIDVLRWNPDDYGGIKVIRVPSDSVWTPDIVLFDNADGRFEGT-STKTV 151
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 MTTNWLKQEWIDVLRWNPDDYGGIKVIRVPSDSVWTPDIVLFDNADGRFEGT-STKTV 140

QY 152 IRYNGTWTTPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDDQVDKRD 211
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 141 VKSGTGVSWTPPASYKSSCTMDVTFPPDLQNCMKFGSWTYDGTWVDLILINENVDKRD 200

QY 212 FPDNGEWEIVSATGSKGNRTDSCCWYPYVTSYFVKRLPFLFYTLFIIPICIGLSFLTIV 271
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 201 FPDNGEWEILNAKGMKNRREGFYSPYFVTSYFVLRRLPFLFYTLFIIPICIGLSFLTIV 260

QY 272 FYLPSNEGEKICLTSLVSLTVFLVIBELIIPSSKVIPLIGELYVFTMFTLSIMVT 331
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 261 FYLPSDEGEKLSLTVSLVSLTVFLVIBELIIPSSKVIPLIGELYVFTMFTLSIIVT 320

QY 332 VFAINIHRSSSTHNAAPLVKIFLHTLPKLLCMRSHVDYF-----TQKEETESGGPK 387
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 321 VFVINVHRSSSTVHPNAPVWKLFLEKLPWLCKDPRDRFSPDGTESKGVGRGKFP 380

QY 388 SSRNT-----LEAALNSIRYITRHKENDVREVEDKFIQVLDRLMFWTF 435
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 381 KKGQTPTSDGERVLVAFLEKASESIRYISRVKKEHFISQVQDKFVAQVLDRIFLWLF 440
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 436 LFVSIIVGSLGLFVPVIYKW 454
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 441 LTASVLGSLVLIIFPALQKW 459
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RESULT 7

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Q9CYK8 PRELIMINARY; PRT; 449 AA.
AC Q9CYK8 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE 5730417K16RIK protein.
GN CHRN3 OR 5730417K16RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schram L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.P.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilmink L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,
RA Hayaishizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AK017571; BAB30812.1; -.
DR MGD; MGI:106212; Chnrb3.
DR InterPro; IPR006201; Neur_chan channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Transmembrane.
SQ SEQUENCE 449 AA; 51281 MW; FFS4824C5DAAC8E7 CRC64;
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Query Match 58.1%; Score 1427.5; DB 11; Length 449;
Best Local Similarity 62.4%; Pred. No. 3.2e-111;
Matches 274; Conservative 66; Mismatches 64; Indels 35; Gaps 5;

QY 33 AORGLSEPSIAKHEDSLKDLFQDYERWVRVPEHLNDKIKIFGLAISQLVDVDEKNQL 92
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 24 ATAGL-----SSVAEHEDALLRHFLFGYQKCVRPVLNSSDIIKVFGLKISQLVDV----- 74

QY 93 MTTNWLKQEWIDVLRWNPDDYGGIKVIRVPSDSVWTPDIVLFDNADGRFEGT-STKTV 151
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 75 -----EWTQDLRWNPEDYGGINSIKVPSSESLWLPDIVLFDNADGRFEGSLMTKAI 125

QY 152 IRYNGTWTTPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDDQVDKRD 211
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 126 VKSGTGVSWTPPASYKSSCTMDVTFPPDLQNCMKFGSWTYDGTWVDLILINENVDKRD 185

QY 212 FPDNGEWEIVSATGSKGNRTDSCCWYPYVTSYFVKRLPFLFYTLFIIPICIGLSFLTIV 271
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 186 FPDNGEWEILNAKGMKNRREGFYSPYFVTSYFVLRRLPFLFYTLFIIPICIGLSFLTIV 245
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QY 272 FYLPSNEGEKICLCTSVLSVLTFTVLVIEEIIIPSSSKVPIPLGEYLVFTMIFTVLSIMVT 331
Db 246 FYLPSDEGEKLSGLSVLSVLTFTVLVIEEIIIPSSSKVPIPLGEYLVFTMIFTVLSIMVT 305
QY 332 VFAINIHRSSSTHNAAPLVKRIKFLHTLPKLLCMRSHVDRYF---TQKEBETESGSPK 387
Db 306 VFVINHRSSSTYHPMAPWVKRLEKLPWLCKMPDRDRSPDPGTHESKGTVRGKFP 365
QY 388 SSRNT-----LEAALNSIRYTRHMKENDREVVEDWKFIAQVLDRLMFLWTF 435
Db 366 KKKQPTSDGERVLVAFLEKASESIRYSRHVKEHFIQVQVDWKFVQVLDRLFLWLF 425
QY 436 LFVSVIGSLGLFVPVIYKW 454
Db 426 LTASVLGSLVLPFIPALKMW 444

RESULT 8
Q91X60 PRELIMINARY; PRT; 512 AA.
ID Q91X60
AC Q91X60
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Similar to cholinergic receptor, nicotinic, alpha polypeptide 2
DE (Neuronal).
GN CHRNA2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; BC011490; AAH11490.1; -.
DR MGD; MGI:87886; Chrna2.
DR InterPro; IPR006201; Neur channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 512 AA; 58735 MW; AC0C6CC398B69C6C CRC64;

Query Match 48.3%; Score 1186.5; DB 11; Length 512;
Best Local Similarity 49.3%; Pred. No. 66-91;
Matches 237; Conservative 73; Mismatches 102; Indels 69; Gaps 7;

QY 37 LSEPSIAKHEDSLKOLFQDYERVWRVPEHLNDKIKFKGLAISQVLDVDEKQNMVTN 96
Db 26 LAQQSHTHAEDRLFKHFGGYNRWAPVPTSDVIVRFGLSIAQLIDVDEKQNMVTN 85
QY 97 VWLKQEWIDVLRNPNDDYGGIKVIRVPSDSVWTPDIVLFONADGRFGT-STKTIVRYN 155
Db 86 VWLKQEWNDYKLRWDPAEFGNITSLRVPSEMIWIDIVLYNNADGEFAVTHMTKAHLFT 145
QY 156 GTVTWTPPANKSSCTIDVTFPPDPLQNCMKFGSWTYDGSQVDIILEDQDVKRDFDN 215
Db 146 GTVHWVPPAIYKSSCIDVTFPPDQCKRKFGSWTYDKAKIDLEQMERTVLDLKYWES 205
QY 216 GEWEIVSATGSGNRDSCC--WYPVYTSYFVKRLPLFTLFLIIPICGLSFLVLFVY 273
Db 206 GEWALINATGYNKSKYDCCAEIYPDVYTFVIRKPLPYINLIIPCLLSCLVLFVY 265
QY 274 LPSNEGEKICLCTSVLSVLTFTVLVIEEIIIPSSSKVPIPLGEYLVFTMIFTVLSIMVT 333
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Db 266 LPSEGEKITICISVLLSLTFLVLLITEIIPSTSLVPLIGEYLLFTMIFTVLSIVITVF 325
QY 334 AINIHRRSSSTHNAAPLVKRIKFLHTLPKLLCMRSHV----- 370
Db 326 VLNVHRSSTPHN-MPNWVRVALLGRVPRWLMNRPPLPMBELHSGPGLKLSPTYHWTN 384
QY 371 ---DRYPTQKEBETES-----GS-----GPKSSRNT----- 392
Db 385 MDABEREETESEEEDENICMCAGLPDSSMGVLYGHSLHRLRANGPEAKTPSQASEIL 444
QY 393 ----LEAALNSIRYTRHMKENDREVVEDWKFIAQVLDRLMFLWTFVSVIGSLGLFV 448
Db 445 LSPQIQKALEGVHYIADHLRSEDADSSVKEDWKYVAMVVDRIFLWFIIVCFGLTGIFL 504
QY 449 P 449
Db 505 P 505

RESULT 9
Q9ET51 PRELIMINARY; PRT; 629 AA.
ID Q9ET51
AC Q9ET51
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 4 subunit.
GN CHRNA4 OR ACR4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Long Sleep Selected Line;
RA Stitzel J.A., Jimenez M., Smolen A., Modir J.;
RT "Cloning of mouse nicotinic acetylcholine receptor subunit alpha 4 cDNA.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF225912; AAF34716.2; -.
DR MGD; MGI:87888; Chrna4.
DR InterPro; IPR006201; Neur channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 629 AA; 70319 MW; 78C28BDEFE371FB2F CRC64;

Query Match 47.0%; Score 1153.5; DB 11; Length 629;
Best Local Similarity 39.8%; Pred. No. 4.6e-88;
Matches 251; Conservative 78; Mismatches 111; Indels 191; Gaps 10;

QY 1 MAARGSPRALRLRLLLVQLVAGRCGLAGAGAGQRLSEPSIAKHEDSLKOLFQDYER 60
Db 88 MEIGSGAPPELLELLLLLLG-TGLLPAS-----SHIETRAHEERLKRFLSGYNK 52
QY 61 WRPVPEHLNDKIKFKGLAISQVLDVDEKQNMVTNVLKQEWIDVLRNPNDDYGGIKV 120
Db 53 WSREPVANISDVLRVFGLSIAQLIDVDEKQNMVTNWVKQEWHDYKLRWDPGDEVNTS 112
QY 121 IRVPSDSVWTPDIVLFONADGRFGT-STKTIVRYNGTVTTPPANKSSCTIDVTFPP 179
Db 113 IRIPSEIWRPDIIVLYNNADGNFAVTHLTKAHLFDGRVQVTPPPIYKSSCIDVTFPP 172
QY 180 DLQNCMKFGSWTYDGSQVDIILEDQDVKRDFDFFDGEWEIVSATGSGNRDSCC--WY 237
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Db 173 DOQNCIMKFGSWTYDQAKIDLVSMSRVDQLDFWESGEWIVDAGVTYNTKRYECAEY 232
Qy 238 PVTYYSFVIRKPLFLYTLFLIIPICIGSLFVLVFLPSNEGEKICLCTSVLVSILTVFLL 297
Db 233 PDITVAFIRRLPLFLYTLFLIIPICISLCTVLVFLPSECEKVTLCISVLSLTVFLL 292
Qy 298 VIEEIIIPSSKVIPIGELVYVMTFVLSIMVTVPAINIHRSSTNNAMAPLVKIKPL 357
Db 293 LITEIIPSTSLVPIGELVYVMTFVLSIMVTVPAINIHRSSTNNAMAPLVKIKPL 351
Qy 358 HTPLKLLCWR-----SHVDRYFTQKE----- 378
Db 352 DIVPRLFLKWRSSVVDKNCRRILIESMHKMANAPRFPWPESPGLIGDIGNGLSPATPF 411
Qy 379 -----ETESGS-----GPKSS----- 389
Db 412 CNRMDTAVETOCTCRSPSHKVPDLKTSEVKASPCSPGSCHPNNSGAPVLKARLSV 471
Qy 390 ---RWLEAALNSIR----- 401
Db 472 QHVPSSQEAAGSIRCSRISIQYCVSQDGAASLTESKPTGSPASLKRPSQLPVSDQTS 531
Qy 402 -----YTRHMKENDVREVE 418
Db 532 CKCTCKEPPSPITVLKAGTKAPQHLPLSPALTRAVEGVQYIADHLKAEDTDFSVKE 591
Qy 419 DWKFIAQVLDRLMFLVFLVSVIGSLGLFVP 449
Db 592 DWKYAVWIDRLFMWFIIVCLLGTGVGLF 622

RESULT 12
Q9ROW9 PRELIMINARY; PRT; 494 AA.
AC Q8VHH6;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor subunit alpha6.
GN CHRA6 OR NICA6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Le Novere N.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Marubio L.M., Champetiaux N., Changeux J.P.;
RT "Cloning of the nicotinic acetylcholine receptor subunit alpha6 from mouse brain.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AJ245706; CAB53472.1; -.
DR MGD; MGI:106213; Chna6.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR Pfam; PF02931; Neur_chan_LBD.
DR Pfam; PF02932; Neur_chan_LBD; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Transmembrane.
SQ SEQUENCE 494 AA; 56807 MW; 650E6CD5CFCD745F CRC64;
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Query Match 46.4%; Score 1139; DB 11; Length 494;
Best Local Similarity 46.8%; Pred. No. 5.5e-87;

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Matches 221; Conservative 92; Mismatches 105; Indels 54; Gaps 8;
Qy 37 LSEPSIAKHEDSLKDLFQDYERWVREHLNDKIKIFGLAISQLVDVDEKNQMTTN 96
Db 24 LFKSGTCESEBEQLFHLFAHYNRFIRPVENVSDPTVHLELAITQLANDEVNQIMETN 83
Qy 97 VWLKQEWIDVKLRNPDYGGIKVIRVPSDSWPTPDIVLFDNADGRF--EGTSTKTVIRY 154
Db 84 LMLRHIMKDYRLRMDPTDYDGIETLRVPADINWKPDIVLYNNVAGDFQVEG-KTKALLKY 142
Qy 155 NGTWTWTPPANKSSCTIDVTFPPDLQNCMSKGSWTYDGSQVDIILEDQDVDRDFD 214
Db 143 DGVITWTPALFKSCPMIDITFPFPHQNCSLKGSWTYDKAIDLLIGSKGMNDFWE 202
Qy 215 NGEWEIVSATGSKGNRTDSCC--WYPYVYTSFVIRKPLFLYTLFLIIPICIGSLTVLVF 272
Db 203 NSEWEIVDASGVKHDIKYNCCEIYDITYSFYIRRLPMFYTLINLIIFCLFISFLTVLV 262
Qy 273 YLPNKGKICLCTSVLVSILVFLVIBEEIIPSSSKVPIPLIGEYLVFTMIFFVLSIMTV 332
Db 263 YLPSCDCEKVTLCISVLSLTVLIVITETIPSTSLVPLVGEYLLFTMIFFVLSIVTV 322
Qy 333 FAINIHRSSTNNAMAPLVKIKPLHTLPLKLCWRSHVDR----- 372
Db 323 FVLNIHYKTPATH-TMPKWVTIIFLAQPPSILMMRKPLDKTKBAGGVKDPKSHTRPAKV 381
Qy 373 YFTQKEETE-----SGSGPKSRNT-----LEAALNSIRYTR 405
Db 382 KFTHRGESKLLKECHCKQSSDIAPGKRSSQOPARWVAENSEHSSDVEDVIESVQFTAE 441
Qy 406 HIMKENDVREVEVDKFIQVLDRLMFLVFLVSVIGSLGLFV-PVIYKWN 456
Db 442 NMKSHNETNEVEDWKYMAWVDRVFLVWFVFIIVCVFVGLFLOPLGLTNGN 493

RESULT 13
Q8VHH6 PRELIMINARY; PRT; 499 AA.
AC Q8VHH6;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Neuronal nicotinic acetylcholine receptor alpha 3 subunit.
GN CHRA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Brain;
RT "Mouse neuronal nicotinic acetyl choline receptor alpha 3 subunit mRNA.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF459029; AAL58471.1; -.
DR MGD; MGI:87887; Chna3.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006029; Neur_chan_LBD.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_LBD; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Transmembrane.
SQ SEQUENCE 499 AA; 57125 MW; D21650F6A6AD7C14B CRC64;
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Query Match 44.7%; Score 1097.5; DB 11; Length 499;
Best Local Similarity 43.2%; Pred. No. 1.7e-83;
Matches 217; Conservative 97; Mismatches 109; Indels 79; Gaps 7;

Qy 8 PRALRLLLLVQVAGRCGLAGAGGAQGLSEPSSTAKHEDSLKDLFQDYERWVRVVEH 67
Db 7 PPPLSMLMLVLM-----LLPVASASEAHLRFQYLFEDYNEIIRVAN 49
Qy 68 LNDKIKIKFGLAISQLVDVDEKNQMTNNVWLKQEWIDVKLRWNPDDYGGIKVIRVPSDS 127
Db 50 VSHPVIIQFEVSNLSQVVKVDEVNQIMETNLWLKQIWNQDKLWKPKSDYQGVBFMRVPAEK 109
Qy 128 VMTPDIVLFDNADGRPE-GTSTKTIVRYNGTWTTPPANYSCTIDVTFPPFDLQNCMS 186
Db 110 IKRPDIVLYNNADGDFQVDDKTALLKYTGCVTWIPPAIFKSSCKIDVTYFPFDYQNCMTM 169
Qy 187 KFGSWTYDGSQVDIILEDQDDVKRDFPDNGEWEIVSATGSKGNRTDSCC--WYPYVTVYSF 244
Db 170 KFGSWSYDKAKIDLVLGSSMNLKDYWESGEWAIKAPGYKHEIKYNCCEIYQDITYSL 229
Qy 245 VIKRLPLFYTLFIIPCLIGLSFLTLVFLYPLSPNEGEKICLCTSVLVSFLVFLVIEEIIIP 304
Db 230 YIRRLPLFYTLINLIIPCLLISFLTLVFLYPLSPDCEKVTLCISVLLSLTVFLVITETIP 289
Qy 305 SSKSVIPLIGEYLVFTMIFVTLSIMVTVFAINIHRRSSSTHNAAPLVKRFILHTLPKLL 364
Db 290 STSLVIPLEGEYLLFTMIFVTLISIVTVFVNLVHYRTPTTH-TMPTWVKAVFLNLLPRVM 348
Qy 365 CMRSHVDVRYFTQKEETESGSGPK----- 387
Db 349 -----FMTPTSTEE-DAPKTRNFYGAELSNLNCFSRADSKSCKEGYPCQDGTGCGYC 399
Qy 388 -----SSRNTLEA-----ALNSIRYITRHKENDVREV 417
Db 400 HHRVVKISNFSANLTRSSSESVDVLSLSALSPEIKAEIQSVKYIAENKQAQVAKIEIQ 459
Qy 418 EDWKVIAQVLDNRFLWTLFVSVIGSLGFV 448
Db 460 DDWKYVAVMVIDRIFLWVFLVLCILGTAGLFL 490

RESULT 15
Q8B44 PRELIMINARY; PRT; 504 AA.
ID Q8B44
AC Q8B44;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Neuronal NICOTINIC acetylcholine receptor alpha 3 subunit.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=22354683; PubMed=12466851;

Qy 8 PRALRLLLLVQVAGRCGLAGAGGAQGLSEPSSTAKHEDSLKDLFQDYERWVRVVEH 67
Db 7 PPPLSMLMLVLM-----LLPVASASEAHLRFQYLFEDYNEIIRVAN 49
Qy 68 LNDKIKIKFGLAISQLVDVDEKNQMTNNVWLKQEWIDVKLRWNPDDYGGIKVIRVPSDS 127
Db 50 VSHPVIIQFEVSNLSQVVKVDEVNQIMETNLWLKQIWNQDKLWKPKSDYQGVBFMRVPAEK 109
Qy 128 VMTPDIVLFDNADGRPE-GTSTKTIVRYNGTWTTPPANYSCTIDVTFPPFDLQNCMS 186
Db 110 IKRPDIVLYNNADGDFQVDDKTALLKYTGCVTWIPPAIFKSSCKIDVTYFPFDYQNCMTM 169
Qy 187 KFGSWTYDGSQVDIILEDQDDVKRDFPDNGEWEIVSATGSKGNRTDSCC--WYPYVTVYSF 244
Db 170 KFGSWSYDKAKIDLVLGSSMNLKDYWESGEWAIKAPGYKHEIKYNCCEIYQDITYSL 229
Qy 245 VIKRLPLFYTLFIIPCLIGLSFLTLVFLYPLSPNEGEKICLCTSVLVSFLVFLVIEEIIIP 304
Db 230 YIRRLPLFYTLINLIIPCLLISFLTLVFLYPLSPDCEKVTLCISVLLSLTVFLVITETIP 289
Qy 305 SSKSVIPLIGEYLVFTMIFVTLSIMVTVFAINIHRRSSSTHNAAPLVKRFILHTLPKLL 364
Db 290 STSLVIPLEGEYLLFTMIFVTLISIVTVFVNLVHYRTPTTH-TMPTWVKAVFLNLLPRVM 348
Qy 365 CMRSHVDVRYFTQKEETESGSGPK-----RSHVDVRYFTQ-----KEET 380
Db 349 FMTPTSTEE-DAPKTRNFYGAELSNLNCFSRADSKSCKEGYPCQDGTGCGYCHRRVVKISN 408
Qy 381 ESGSGPKSSN-----TLEAALNSIRYITRHKENDVREVVEDWKFTAQV 426
Db 409 FSNALTRSSSESVDVLSLSALSPEIKAEIQSVKYIAENKQAQVAKIEIQDDWKYVAVM 468
Qy 427 LDRMFLWTLFVSVIGSLGFV 448
Db 469 IDRIFLWVFLVLCILGTAGLFL 490

RESULT 14
Q8R4G9 PRELIMINARY; PRT; 499 AA.
ID Q8R4G9
AC Q8R4G9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor alpha 3 subunit.
GN CHRNA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DEA/21bg; TISSUE=Adrenal gland;
RA Lautner M.A., Scitzel J.A.;
RT "Cloning of mouse nicotinic acetylcholine receptor alpha 3 subunit
cDNA."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion, and Eye;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF472588; AAL84757.1; --
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RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
DR EMBL: AK080415; BAC37809.1; -.
SQ SEQUENCE 504 AA; 57686 MW; CSBBSOPF4DEI5ECD C RC64;

Query Match          44.7%; Score 1097.5; DB 11; Length 504;
Best Local Similarity 42.5%; Pred. No. 1.7e+83;
Matches 217; Conservative      95; Mismatches 102; Indels   97; Gaps    28;

QY  8 PRAIRLLLLVLVAGRCGLAGAGAAGGAGLSEPSIAKHEDSLKLQFDYERWRVPVEH 67
DB  12 PPPLSMLMLVLM-----LLPVASASEAESHRLFQYLFDYNEIIRPVAN 54
QY  68 LNDKIKTKFGLAISQLVDDEKNOLMTTNWLVKGWEIDVKLRNPDYGIGIKVRPSPDS 127
DB  55 VSHPIVIQFEVSMSQLKYDVENQMIMETNLWLKQINWDYKLWKPKPSDYQGVEPMRVPAEK 114
QY 128 VWTPDDIVLPONADGRPP-GTSTKTIVIRYNGTVTWTPPANVKSCTIDVTFFPDLQNCSM 186
DB 115 IWKPPDIVLYNNADGFQDDKTKALLXKIGEVTIWPPAIKSSCKCIDVTIFFPDYQNCNM 174
QY 187 KFGSWTYDGSDQVDIIILDQBDVKRDFPDNGEWEIVSATSGKNRTDSCC--WYPYVITYSF 244
DB 175 KFGSWSYDKAKIDLVLIGSSMWLNKYWESGEWALIKAPGYKHEIKYNCCBEIQDITYSL 234
QY 245 VIKRPLPYFTFLIIPICIGLSFUTVLVVFYLPNSNEGKICLCISVLVSLTVFLVLVIEIIP 304
DB 235 YIRRPLPFYFINLIIPCILISFLTIVLVFYLPSCGEKVTLCSVLLSLTVFLVLVITETIP 294
QY 305 SSKSVYPLIGEYLVFTMIFTLISMTVTFVAINIHRRSSSTHNAMAPLVRKIFLHTLPKLL 364
DB 295 STLVLPIIGEYLLFTMIFTLISIVTFVLNVHYRTPTTH-TMPTWVKAVFLNLLPRVM 353
QY 365 CMRSHVDVRYFTQKEETEGSGGPK-----387
DB 354 -----FWMRPTSTEE-DAPKTRPNFYGAELSNLNCFSRADSKSKGEPQQDTGCYC 404
QY 388 -----SSRNITLEA-----ALNSRYITRIHKENDVREVV 417
DB 405 HHRRVKISFNPSANLTRSSSESSEDAVLSSLSPAISPEIKEALQS VKYIAENMKAAQNVAKEIQ 464
QY 418 EDWKFTAQVLDRLMFLWTFLFVSVIVGSIGLGV 448
DB 465 DDWKYVAMVIDRIFLWVFIWVICILGTAGLE 495

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 18:47:38 ; Search time 24 Seconds
(without alignments)
917.021 Million cell updates/sec

Title: US-09-703-951A-8

Perfect score: 2456

Sequence: 1 MAARGSPRALRLLLVQLV.....PVIYKWNILIPVHGNANK 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2451	99.8	468	1 ACH5 HUMAN	P30532 homo sapien
2	2148.5	87.5	452	1 ACH5_RAT	P20420 rattus norv
3	2034	82.8	454	1 ACH5_CHICK	P26152 gallus gall
4	1586	64.6	458	1 ACHO HUMAN	Q05901 homo sapien
5	1579.5	64.3	462	1 ACHO CARAU	P13908 carassius a
6	1568.5	63.9	455	1 ACHO CHICK	P43679 gallus gall
7	1534	62.5	464	1 ACHO_RAT	P12391 rattus norv
8	1531	62.3	466	1 ACHP_CARAU	P18257 carassius a
9	1201.5	48.9	529	1 ACH2 HUMAN	Q15822 homo sapien
10	1179	48.0	511	1 ACH2_RAT	P12389 rattus norv
11	1166.5	47.5	528	1 ACH2_CHICK	P09480 gallus gall
12	1157.5	47.1	627	1 ACH4 HUMAN	P43681 homo sapien
13	1143	46.5	512	1 ACH3 CARAU	P18845 carassius a
14	1142.5	46.5	630	1 ACH4_RAT	P09483 rattus norv
15	1139	46.4	493	1 ACH6_RAT	Q15825 homo sapien
16	1135	46.2	494	1 ACH6 HUMAN	P43143 rattus norv
17	1129.5	46.0	622	1 ACH4 CHICK	Q15825 homo sapien
18	1119.5	45.6	494	1 ACH6 CHICK	P09482 gallus gall
19	1116.5	45.5	495	1 ACH3 BOVIN	P49581 gallus gall
20	1114	45.4	496	1 ACH3_CHICK	Q07263 bos taurus
21	1112	45.3	503	1 ACH3 HUMAN	P09481 gallus gall
22	1096.5	44.6	499	1 ACH3_RAT	P32297 homo sapien
23	1028.5	41.9	498	1 ACHP HUMAN	P04757 rattus norv
24	1025.5	41.8	567	1 ACH1 DROME	P09478 drosophila
25	1024	41.7	516	1 ACH1_MANSE	P91766 manduca sex
26	1020.5	41.6	456	1 ACHA_CHICK	P09479 gallus gall
27	1020	41.5	519	1 ACH4 DROME	P25162 drosophila
28	1019.5	41.5	457	1 ACHA_MOUSE	P04756 mus musculu
29	1016	41.4	495	1 ACHP_RAT	P12392 rattus norv
30	1012	41.2	457	1 ACHA_BOVIN	P02709 bos taurus
31	1009.5	41.1	457	1 ACHA_RAT	P25108 rattus norv
32	1000	40.7	557	1 ACH1_SCHGR	P23414 schistosom
33	998	40.6	461	1 ACHA_TORMA	P02711 torpido mar

RESULT 1

ACH5_HUMAN

ID ACH5_HUMAN STANDARD; PRT; 468 AA.

AC P30532; Q15824; Q99554;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuronal acetylcholine receptor protein, alpha-5 chain precursor.

GN CHRNA5 OR NACHRA5

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=92179225; PubMed=1543648;

RA Chini B., Clementi F., Hukovic N., Sher E.;

RT "Neuronal-type alpha-bungarotoxin receptors and the alpha 5-nicotinic receptor subunit gene are expressed in neuronal and nonneuronal human cell lines";

RL Proc. Natl. Acad. Sci. U.S.A. 89:1572-1576(1992).

RN (2)

RP SEQUENCE FROM N.A.

RX MEDLINE=97062879; PubMed=8906617;

RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,

Chavez-Noriega L.E., Johnson E.C., Velicellebi G., Harpold M.M.;

RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits";

RL J. Mol. Neurosci. 7:217-228(1996).

RN (3)

RP SEQUENCE FROM N.A.

RX MEDLINE=97162233; PubMed=9009220;

RA Groot Kormelink P.J., Luyten W.H.M.L.;

RT "Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32";

RL FEBS Lett. 400:309-314(1997).

RN (4)

RP SEQUENCE FROM N.A.

RA Duga S., Solda G., Asselta R., Bonati M.T., Dalpra L., Malcovati M.,

Tenchini M.L.;

RT "Characterization of the genomic structure of human nicotinic acetylcholine receptor CHRNA5/A3/B4 gene cluster: identification of two novel introns in the 3' untranslated region of CHRNA3 and of a tail-to-tail overlap between CHRNA3 and CHRNA5";

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.

CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC

J. Biol. Chem. 265:17560-17567(1990).

-!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.

-!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND THREE NON-ALPHA CHAINS.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

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Matches	3/8; Conservative	30; Mismatches	35; Indels	0; Gaps	0
QY	25	GLAGAGGAQGRGLSEPSIAKHEDSLIKDLFDQYERWRVPVEHLNDKIKFKGLAISQLV	84		
Db	11	GAGPAARAQAQGVSEPSFVAKSEDLRFKHLFEDYQRWRVPVEHLNDTIKFKGLAISQLV	70		
QY	85	DVDEKNQLMTTNVWLKQEWIDVKLRNPDYGGIKVIRVPSDSVWTVPDIVLFNADGRFE	144		
Db	71	DVDEKNQLMTTNVWLKQEWIHVKLRNPDYAGITSIRVPSDSITWIPDIVLYFNADGRFE	130		
QY	145	GTSTKTVIRYNGVTWTPPANKYSSCTIDVTPEPFDLQNCMKFGSWTYDGSQVDIILE	204		
Db	131	GTSTKTVIRYKIDGTIAWTPPNKYSSCTIDVTPEPFDLQNCMKFGSWTYDGSQVDIILE	190		
QY	205	QVDKRDPDFDNGEWEIVSATSGKGNRTDSCWYPVYTVSFVIKRLPLFTFLIIPICGL	264		
Db	191	YEVDKRDPDFDNGEWEIVTATSGKGNRTDGCWYPFVTVSFIIIRRLPLFTFLIIPICGL	250		
QY	265	SFLTVLVFLVLPNNEGEKICLCTSVLVSLTVFLVIEEIIIPSSSKVPIPLIGEYLVFTWIFV	324		
Db	251	SFLTVLVFLVLPNNEAEKISLCTSVLVSLTVFLVIEEIIIPSSSKVPIPLIGEYLVFTWIFV	310		
QY	325	TLISIMVTFAINIHRRSSSTHNAMAPLVKFIHLHTLPKLLCMRSHVDVRYPTOKBETESGS	384		

[illegible]

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: RELATIVELY ABUNDANT IN THE DEVELOPING RETINA
 CC AND IN THE TRIGEMINAL GANGLION.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X83739; CAB59814.1; -;
 DR PIR; A55972; A55972.
 DR InterPro; IPR006029; Neu channel memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_chan_LBD.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_LBD; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 455 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT BETA-3 CHAIN.
 FT DOMAIN 21 229 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 230 254 POTENTIAL.
 FT TRANSMEM 262 279 POTENTIAL.
 FT TRANSMEM 296 317 POTENTIAL.
 FT DOMAIN 318 425 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 426 444 POTENTIAL.
 FT DISULFID 150 164 BY SIMILARITY.
 FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 455 AA; 52276 MW; 3D7A7AFA77D8511A CRC64;

 Query Match 63.98; Score 1568.5; DB 1; Length 455;
 Best Local Similarity 67.6%; Pred. No. 7e-122;
 Matches 292; Conservative 61; Mismatches 62; Indels 17; Gaps 3;

 QY 42 SIARHEDSLKDLFQDYERWVRPVEHLNDKIKFKGLAISQLVDVDEKNQMTTNWLKQ 101
 DB 21 SVVENEDALLRHLPFGQYQKWRVPVENSNDIKVLFGLKISQLVDVDEKNQMTTNWLKQ 80
 QY 102 EWIDVLRWNPDDYGGIKVIRVPSDSVWTPDIVLFDNADGRPEGT-STKTVIRYNGVTW 160
 DB 81 EWMHDKLSWNPDEYGGITAIRVPSDSLWLPDIVLFENADGRFEGSLMTKAIVKYNQVQW 140
 QY 161 TTPANYKSSCTIDVTFPPFDLONCSMKFGSWTVDGSDVILDEDVDKDFDNGEWI 220
 DB 141 MPPASYKSSCTMELTFPPFDQNCMSKFGSWTVDGSMVDLILVDENVDTKDFDNGEWI 200
 QY 221 VSGTSGKGNRTDSCWPPYTYTSVKIRLPLFTFLIIPICIGLSPLTVLVFVLPNSGE 280
 DB 201 LNAKGMKGNKRGGLYSFPVTFYFVLRRLPLFTFLIIPICIGLSPLTVLVFVLPNSGE 260
 QY 281 KICLCTSVLSVTLVFLVIEEIIIPSSSKVPIIGELVLFVTFMIFVLSIMVTVFAINHR 340
 DB 261 KLSLSTSVLSVTLVFLVIEEIIIPSSSKVPIIGELVLFVTFMIFVLSIIVTVFVNVHR 320
 QY 341 SSSTHNAAPLVKIKFLHTLPLKLCMRSHVDY-FTQKEETE-----SGS 384
 DB 321 SSATYHPMAPWVRLFLQKLPRLCLMKGHVDRYSFSDTEETKTLKSLPGKQKQAKD 380
 QY 385 GPKSSRRTLAALNSIRYTRHMKENDVREWEDKFIQVLDRLMFLWTFVLSVIGSL 444
 DB 381 GEKVVIATFLKADSIIRYISRHVKQDAFIRQVQVDKFWAQVLDRIPLWFLVLSVTVGSV 440
 QY 445 GLFVPIYIKWAN 456
 : : : : :

Db 441 LIPTPALQMWLN 452
 RESULT 7
 ACHO RAT STANDARD; PRT; 464 AA.
 AC P12391;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, beta-3 chain precursor.
 GN CHRN3 OR ACRB3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89197926; PubMed=2703489;
 RX Deneris E.S., Boulter J., Swanson L.W., Patrick J., Heinemann S.F.;
 RT "Beta 3: a new member of nicotinic acetylcholine receptor gene family
 is expressed in brain.";
 RL J. Biol. Chem. 264:6268-6272(1989).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT. NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
 CC TYPES OF SUBUNITS: ALPHA AND BETA.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J04636; AAC28887.1; -;
 DR PIR; A33523; A33523.
 DR InterPro; IPR006029; Neu channel memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_chan_LBD.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_LBD; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMs; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 464 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT BETA-3 CHAIN.
 FT DOMAIN 31 238 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 239 263 POTENTIAL.
 FT TRANSMEM 271 288 POTENTIAL.
 FT TRANSMEM 305 326 POTENTIAL.
 FT DOMAIN 327 434 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 435 453 POTENTIAL.
 FT DISULFID 159 173 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 464 AA; 53261 MW; 5D3B1F7DB934D1D8 CRC64;

 Query Match 62.5%; Score 1534; DB 1; Length 464;
 Best Local Similarity 65.1%; Pred. No. 5.1e-119;
 Matches 286; Conservative 71; Mismatches 62; Indels 20; Gaps 3;

 QY 33 AORGLSEPSIAKHEDSLKDLFQDYERWVRPVEHLNDKIKFKGLAISQLVDVDEKNQ 92
 DB 24 ATAGL---SSVAEHEDALLRHLPFGQYQKWRVPVLSNDSIIKVFGLKISQLVDVDEKNQ 80
 : : : : :

QY 93 MTTNVLKQEWIDVLRNPDYGGIKVIRVPSDSVWTPDVLVFNADGRFEGT-STKTV 151
Db 81 MTTNVLKQEWTDQKLRNPEYGGINSIKVPSLSLWLPDVLVFNADGRFEGSLMTKAI 140
QY 152 IRYNGTWTTPANKSSCTIDVTFPPDLQNSMKFGSWTYDGSQVLDLIDQVDKRD 211
Db 141 VSSSTVWTPPASYSKCTMDVTFPPDRQNSMKFGSWTYDGTWDLILINENVDKRD 200
QY 212 PFDNGEIVSAGSKGRTSCCWPYVTVSVFKIRLPFLFYLFLIIPICIGLSPLTVLV 271
Db 201 PFDNGEIVSAGSKGRTSCCWPYVTVSVFKIRLPFLFYLFLIIPICIGLSPLTVLV 260
QY 272 FYLPNBEKICLCTSVLSVLTFLVFLVIEEIPSSSKVPIPLIGEVLVFTMIFVTLISIMVT 331
Db 261 FYLPNBEKICLCTSVLSVLTFLVFLVIEEIPSSSKVPIPLIGEVLVFTMIFVTLISIMVT 320
QY 332 VFAINIHRSSTHNAAPLVKIRKIFLHTLPKLLCMRSHVDY-FT 375
Db 321 VFAINIHRSSTHNAAPLVKIRKIFLHTLPKLLCMRSHVDY-FT 360
QY 376 QKEETESGPKSSNTLEAALNSIRYITRHKMKENDVREVEDWKFIAQVLDRLMFLWTF 435
Db 361 KKKQTPASDGERVLVAFLEKASESIRYISRHVKKEHFISQVQDWKFAQVLDRLMFLWTF 440
QY 436 LFVSVGLFGLFVPIYK 454
Db 441 LIASVLGSLIFIPALK 459

RESULT 8

ACHP_CARAU STANDARD; PRT; 466 AA.
AC P18257;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, non-alpha-3 chain precursor (GN-alpha-3).
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Retina;
RX MEDLINE=90155434; PubMed=2303867;
RA Cauley E.A., Agranoff B.W., Goldman D.J.;
RT "Multiple nicotinic acetylcholine receptor genes are expressed in goldfish retina and tectum."
RL J. Neurosci. 10:670-683(1990).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.
CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: RETINA, TECTUM AND BRAIN.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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CC -----
DR EMBL; M29529; AAA49167.1; -;
DR PIR; S16333; S16333.
DR InterPro; IPR006029; Neu_channel_memb.

DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRPFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
FT Transmembrane; Multigene family.
FT SIGNAL 1 28
FT CHAIN 29 466
FT DOMAIN 29 235
FT TRANSMEM 236 260
FT TRANSMEM 268 285
FT TRANSMEM 302 323
FT TRANSMEM 324 438
FT TRANSMEM 439 456
FT DISULFID 156 170
FT CARBOHYD 54 54
FT CARBOHYD 141 141
FT CARBOHYD 169 169
FT CARBOHYD 208 208
SQ SEQUENCE 466 AA; 53801 MW; 3ED8C870CC955F8 CRC64;

NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
NON-ALPHA-3 CHAIN.
EXTRACELLULAR.

CYTOPLASMIC.

BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (PROBABLE).
N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 62.3%; Score 1531; DB 1; Length 466;
Best Local Similarity 64.8%; Pred. No. 9e-119;
Matches 283; Conservative 63; Mismatches 67; Indels 24; Gaps 3;

QY 42 SIAGHEDSLKDLFDQYERWVRVPEHLNDKIKIFGLAISQVLDVDEKQMLTNNVWLKQ 101
Db 27 SLAEMEDTLRLNFRGQKWRPILHANDTITVRFGKISQVLDVDEKQMLTNNVWLWQ 86

QY 102 EWIDVLRNPDYGGIKVIRVPSDSVWTPDVLVFNADGRFEGT-STKTVIRYNGTWTM 160
Db 87 EWTYKLRNPDYGGITSRVPSSETIWLPIVFNADGRFEGSLMTKALVFNGTIMW 146

QY 161 TPPANYKSSCTIDVTFPPDLQNSMKFGSWTYDGSQVLDLIDQVDKRDFFDNGEWEL 220
Db 147 TPPASYKSSCTMDVTFPPDRQNSMKFGSWTYDGTWDLTLLDAYVDRKDFDNGEWEL 206

QY 221 VSATGSKGNRTSCCWPYVTVSVFKIRLPFLFYLFLIIPICIGLSPLTVLVFVLPNBE 280
Db 207 LNATGQGRSDGIYSYVTVSVFKIRLPFLFYLFLIIPICIGLSPLTVLVFVLPNBE 266

QY 281 KICLCTSVLSVLTFLVFLVIEEIPSSSKVPIPLIGEVLVFTMIFVTLSTMTVFAINIH 340
Db 267 KLLSTSVLSVLTFLVFLVIEEIPSSSKVPIPLIGEVLVFTMIFVTLSTMTVFAINIH 326

QY 341 SSSHTNAPLVKIRKIFLHTLPKLLCMRSHVDY-FTQKEETES 382
Db 327 SSATYHPAPWVKSFLFLQRLPRLLCMGHTDRYQYDIELRSPKRMKGQKQKSGG 386

QY 383 GSGPKSSRN-----TLEAALNSIRYITRHKMKENDVREVEDWKFIAQVLDRLMFLW 437
Db 387 RGGLKEDENQAWIALEKATHSVHYISRHVKKEHFIREVQDWKFAQVLDRLMFLW 446

QY 438 VSIIVGSLFGLFVPIYK 454
Db 447 ASVLGTLITFPALHMY 463

RESULT 9

ACH2_HUMAN STANDARD; PRT; 529 AA.
AC Q15822; Q9HAQ3;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
GN CHRNA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


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274 QY LPSNGEKICICTSVLSVLTIVELLVTEETIIPSSSKVPIPLIGEVLTMTIIVTISIMVTVF 333
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334 QY AINIHRSRSTNANAPLVRKIFLHTLPKLLCWRSHV----- 370
326 DB VLVNHRSPSTN-PPNWTVRVALLGRVPRWLMNMRPLPMELHGSDDLKLSPSYHWLETN 384
371 QY -----DRYFTQKQETESGSG-----PKSSRNLT----- 393
385 DB MDAGEREETEEEEEDENICVACGLPDSMGVLVYGHGGLHLRAMEPETKTPQASEILL 444
394 QY ----BAALNISYIYTHINKENDREVVEDKFAIQVDRMLFWLTFLFVIVCSGLGFVFP 449
445 DB SPOIQKALEGVHYIADRLASEDADSVKEDWKYVMVVDRIPLWLFIIIVCFGLTIGLFLP 504

RESULT 11
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AC P09480;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
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SEQUENCE FROM N.A.
TI TISSUE=Brain;
MEDLINE=88283624; PubMed=3267226;
RA Nef P., Onysysz C., Alliod C., Couturier S., Ballivet M.;
RT "Genes expressed in the brain define three distinct neuronal
RL nicotinic acetylcholine receptors."
RL EMBO J. 7:595-601(1988).
CC -! FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -! SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A
CC FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND
CC THREE NON-ALPHA CHAINS.
CC -! SUBCELLULAR LOCATION: Integral membrane protein.
CC -! SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
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CC EMBL; X07474; CAB596
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RL Nucleic Acids Res. 18:5293-5293 (1990).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
 CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
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 CC EMBL; X54051; CAA37985.1; -;
 DR PIR; S11230; B37014.
 DR InterPro; IPR006029; Neu channel memb.
 DR InterPro; IPR006202; Neu_chan_LBD.
 DR InterPro; IPR006201; Neu_chan_LBD.
 DR Pfam; PF02931; Neu_chan_LBD; 1.
 DR Pfam; PF02932; Neu_chan_LBD; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGR; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 512 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT DOMAIN 24 232 ALPHA-3 CHAIN.
 FT TRANSMEM 233 257 EXTRACELLULAR.
 FT TRANSMEM 265 283 CYTOPLASMIC.
 FT TRANSMEM 299 320
 FT DOMAIN 321 485
 FT TRANSMEM 486 505
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 FT DISULFID 215 216
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 FT CARBOHYD 164 164 (BY SIMILARITY).
 FT SEQUENCE 512 AA; 58095 MW; 8D2F63E37CE9077 CRC64;
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 DB 3 SASRITLFFLLTLVITQEC-----LS-----SKGEDRLRRLRFRYNQFIRPV 45
 QY 66 EHLNDKIKIFGLAISQVLDVDEKNQVMTNVLKQEWIDVLRWNPDDYCGGKIVRVP 125
 DB 46 ENVSDDPTVFEVSISQVVKVDEVNQIMETNLRLHNDYKWLPAEFDGIEFIRVP 105
 QY 126 DSVWTPDIVLFDNADGRF-EGTSTKTVIRNGTVTPPPANYKSSCTIDVTFPFDLQNC 184
 DB 106 NKIWRPDIVLYNNAVGDFVEDKTKALKYDGTITVWPPAIFKSSCPMDITYPPFDYQNC 165
 QY 185 SMKFGSTYDGSQVDITLEDQDDVDRDPFDNGEWEIVSAGTSGKGNRTDCC--WYPVVTV 242
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QY 363 LLCMRSHVDYRFTQ-----376
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 QY 377 -----KEETESGSGPKSSRNTELEA-----ALNSRYITRTHM 408
 DB 405 EGKKGCGCPCHPIKEAIEGDCGVSRQLTPQAINTVVTFVSWSPKQAIKESVKYIAENMR 464
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 DB 465 SRNKAKEVEDDDWKVAVWIDRIFLWVFLVGVGLGLFLQFLI 508
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 ID ACH4_RAT STANDARD; PRT; 630 AA.
 AC P09483; O35769;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-4 chain precursor.
 GN CHRNA4 OR ACRA4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 RC STRAIN=Sprague-Dawley; TISSUE=Hippocampus, and Hypothalamus;
 RX MEDLINE=87159533; PubMed=3829125;
 RA Goldman D.J., Deneris E.S., Luyten W., Kochhar A., Patrick J.,
 RA Heinemann S.F.;
 RT "Members of a nicotinic acetylcholine receptor gene family are
 RT system.";
 RL Cell 48:965-973 (1987).
 RN [2]
 RP REVISIONS.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RA Hartley M., Goldman D.J., Heinemann S.F.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Boulter J., Deneris E.S., Evans K., Heinemann S.F.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP PARTIAL SEQUENCE OF 31-47.
 RX MEDLINE=87276531; PubMed=3609304;
 RA Whiting P., Esch F., Shimasaki S., Lindstrom J.;
 RT "Neuronal nicotinic acetylcholine receptor beta-subunit is coded for
 RT by the cDNA clone alpha 4.";
 RL FEBS Lett. 219:459-463 (1987).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-4 SUBUNIT CAN BE
 CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
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 CC Name=Alpha-4-2;
 CC IsoId=P09483-2; Sequence=VSP 000074;
 CC -1- TISSUE SPECIFICITY: IN VARIOUS REGIONS OF THE CENTRAL NERVOUS
 CC SYSTEM.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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OM protein - protein search, using sw model

Run on: December 23, 2003, 20:50:42 ; Search time 37 Seconds
(without alignments)
1216.404 Million cell updates/sec

Title: US-09-703-951A-8
Perfect score: 2456
Sequence: 1 MAARGSPRALRLLLVQLV.....PVIYKANILIPVHIGNANK 468
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2365	96.3	468	2 A38223	nicotinic acetylch
2	2148.5	87.5	452	2 A35721	nicotinic acetylch
3	2047	83.3	454	2 B39218	nicotinic acetylch
4	1579.5	64.3	462	2 S08893	nicotinic acetylch
5	1574.5	64.1	455	2 S51116	nicotinic acetylch
6	1568.5	63.9	455	2 A55972	nicotinic acetylch
7	1534.5	62.5	423	2 I38056	nicotinic acetylch
8	1534	62.5	464	2 A33523	nicotinic acetylch
9	1531	62.3	466	2 S36333	nicotinic acetylch
10	1184	48.2	511	2 A40110	nicotinic acetylch
11	1166.5	47.5	528	1 AACHN	nicotinic acetylch
12	1157.5	47.1	627	2 JCA021	nicotinic acetylch
13	1145	46.6	625	2 A26456	nicotinic acetylch
14	1143	46.5	512	2 B37014	nicotinic acetylch
15	1133.5	46.2	494	2 T09289	nicotinic acetylch
16	1129.5	46.0	622	1 AACHN	nicotinic acetylch
17	1116.5	45.5	495	2 S60589	acetylcholine rece
18	1114.5	45.4	503	2 A53956	nicotinic acetylch
19	1102.5	44.9	502	2 A37040	nicotinic acetylch
20	1096.5	44.6	499	2 A24572	nicotinic acetylch
21	1028.5	41.9	498	2 G02421	nicotinic acetylch
22	1022.5	41.6	567	1 ACFPA1	nicotinic acetylch
23	1020.5	41.6	456	1 AACHN	nicotinic acetylch
24	1016.5	41.4	457	2 A24383	nicotinic acetylch
25	1014	41.3	457	1 ACHUA1	nicotinic acetylch
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27	1012	41.2	457	1 ABOA1	nicotinic acetylch
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29	1009.5	41.1	457	2 S13872	nicotinic acetylch

30	1007	41.0	495	2 B35721	nicotinic acetylch
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33	994	40.5	459	2 S14703	nicotinic acetylch
34	991	40.4	457	2 A28529	nicotinic acetylch
35	990	40.3	576	1 ACFPA2	nicotinic acetylch
36	989.5	40.3	517	2 A30992	probable nicotinic
37	987	40.2	461	1 ACRYA1	nicotinic acetylch
38	984	40.1	502	2 S10505	nicotinic acetylch
39	977.5	39.8	457	2 S08162	nicotinic acetylch
40	977.5	39.8	491	1 ACHNN	nicotinic acetylch
41	975	39.7	503	2 JH0174	nicotinic acetylch
42	972.5	39.6	470	2 A39218	nicotinic acetylch
43	963	39.2	416	1 AACHN	nicotinic acetylch
44	926	37.7	511	2 T43634	nicotinic acetylch
45	904.5	36.8	534	2 T25720	hypothetical prote

ALIGNMENTS

RESULT 1

A38223
nicotinic acetylcholine receptor alpha-5 chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: A38223
R:Chini, B.; Clementi, F.; Hukovic, N.; Sher, E.
Proc. Natl. Acad. Sci. U.S.A. 89, 1572-1576, 1992
A:Title: Neuronal-type alpha-bungarotoxin receptors and the alpha 5-nicotinic receptor
A:Reference number: A38223; MUID:92179225; PMID:1542648
A:Accession: A38223
A:Molecule type: mRNA
A:Residues: 1-468 <CHI>
A:Cross-references: GB:M83712; NID:g177925; PIDN:AA58357.1; PID:g177926
A:Experimental source: IMR32 neuroblastoma cell line
A>Note: sequence extracted from NCBI backbone (NCBI:853377, NCBI:853378)
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-468/Product: nicotinic acetylcholine receptor alpha-5 chain #status predicted <MAT>
F:251-275/Domain: transmembrane #status predicted <TM1>
F:282-304/Domain: transmembrane #status predicted <TM2>
F:310-335/Domain: transmembrane #status predicted <TM3>
F:422-447/Domain: transmembrane #status predicted <TM4>
F:155,183,229/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match
Best Local Similarity 96.3%; Score 2365; DB 2; Length 468;
Matches 454; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy	1	MAARGSPRALRLLLVQLVAGRCGLAGAGGAGRGISEPSSIAKHEDSLKDLFPDYER	60
Db	1	MAARGSPRALRLLLVQLVAGALRRARRARGLSEPSSIAKHEDSLKDLFPDYER	60
Qy	61	WVRPEHLNDIKIKFGLAISQLVDDEKQMLTNNVWLKQEWIDVKLRWNPDDYGGIKV	120
Db	61	WVRPEHLNDIKIKFGLAISQLVDDEKQMLTNNVWLKQEWIDVKLRWNPDDYGGIKV	120
Qy	121	IRVPSDSVWTPDVLFDNADRGFGSTKTVIRYNGTVTTPPPANYKSSCTIDVTFFPFD	180
Db	121	IRVPSDSVWTPDVLFDNADRGFGSTKTVIRYNGTVTTPPPANYKSSCTIDVTFFPFD	180
Qy	181	LQNCMKFGSWTYDGSQVDIILEDQVDKDRFPDNGWEIIVSATGSKGNRTDSCCWYPYV	240
Db	181	LQNCMKFGSWTYDGSQVDIILEDQVDKDRFPDNGWEIIVSATGSKGNRTDSCCWYPYV	240
Qy	241	TYSVVKRLPYTLFLIIPICIGSLFVLVFLPSNEGEKICLCTSVLSLTVFLVLVIE	300
Db	241	TYSVVKRLPYTLFLIIPICIGSLFVLVFLPSNEGEKICLCTSVLSLTVFLVLVIE	300
Qy	301	ETIIPSSSKVPIGLGEVLVFTMIFVTLTSMVTVFAINTIHRSSSTHNAAPLVKIFLHTL	360

QY	161	TPPANTKSC	CTIDVTFFPFDLQNSCMKFGSWTYDGSQVDIILEDQDDVKDRFFDNGEW	220
Db	141	MPASYSK	SCMTLFTFFPDRQNSCMKFGSWTYDGSVDLLVDENVDTKDFDNGEW	200
QY	221	VSATSGK	NRDSCCHWYPTYSFVKRLPLFTFLIIICIGLSPLTVLYFLPSNEGE	280
Db	201	LNAGKMG	KNRKGLGYPFVFTYSFLRRLPLFTFLIIPCGLSFLTVLYFLPSDEGE	260
QY	281	KICLCTSV	LSVLSLTVFLVLVIEIIPSSSKVIPLIGEYLVFTMI FVTLSIMTVFAINIHR	340
Db	261	KLSLSTSV	LSVLSLTVFLVLVIEIIPSSSKVIPLIGEYLLFTMI FVTLSIIVTVFVINVHR	320
QY	341	SSSTHNAM	APLVKRIFLHTLPKLLCMRSHVDYR-FTQKEETE-----SGS	384
Db	321	SSATYHPM	APLVKRLFLQKLPRLLCMKGHVDRYSFSDEBETKTLKSLPGKQKHQAKD	380
QY	385	GPKSSRNT	LEAALNSIRYITRHTIMKENDVPEVVEDKWFIAQVLDRMFLWTFLFVSI	444
Db	381	GEKVITAF	LEKAADSIRYISRHVKQDAFIRQVVQDMKFVAQVLDRIFLWLFLVSVTGSV	440
QY	445	GLFPVPVI	YRKWAN 456	
Db	441	LIFTPALQ	MWLN 452	
RESULT	6			
A:Species	A55972			
C:Species	Gallus gallus (chicken)			
C:Date	03-Oct-1995	#sequence_revision	03-Oct-1995	#text_change 21-Jul-2000
C:Accession	A55972			
R: Hernandez, M.C.; Erkman, L.; Matter-Sadzinski, L.; Roztocil, T.; Ballivet, M.				
J. Biol. Chem.	270, 3224-3233, 1995			
A:Title	Characterization of the nicotinic acetylcholine receptor beta3 gene.			
A:Reference number	A55972; MUID:95155414; PMID:7852408			
A:Accession	A55972			
A>Status	preliminary			
A:Molecule type	DNA			
A:Residues	1-455	<HER>		
A:Cross-references	GB:X87339; NID:G6165256; PIDN:CAB59814.1; PID:G6165257			
C:Superfamily	acetylcholine receptor			
C:Keywords	neurotransmitter receptor			

[illegible]

Db 381 GERVIAFLKAADSIRYSRHVKDAFIRQVQDWFKAQVLDRIFLMLFLVSVTGSV 440
QY 445 GLFVPVVIYKWN 456
Db 441 LIPTPALQWLN 452

RESULT 7
I38056
nicotinic acetylcholine receptor beta-3 chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 20-Aug-1999
R:Willoughby, J.J.; Ninkina, N.N.; Beech, M.M.; Latchman, D.S.; Wood, J.N.
Neurosci. Lett. 155, 136-139, 1993
A:Title: Molecular cloning of a human neuronal nicotinic acetylcholine receptor beta 3-1
A:Reference number: I38056; MUID:93390761; PMID:7690916
A:Accession: I38056
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-423 <RES>
A:Cross-references: EMBL:X67513; NID:934987; PIDN:CAA47851.1; PID:934988
C:Genetics:
A:Gene: GDB:CHRN3; ACHR
A:Cross-references: GDB:125222; OMIM:118508
A:Map position: 8p11.2-8p11.2
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor

Query Match 62.5%; Score 1534.5; DB 2; Length 423;
Best Local Similarity 68.6%; Pred. No. 1.6e-118;
Matches 286; Conservative 57; Mismatches 57; Indels 17; Gaps 3;

QY 55 FQYERWRVPVEHLNDKIKIFGLAISQVVDVDEKQNLMTTNVWLKQEWIDVKLRWNPDD 114
Db 2 WKGYQKWRVPVLSNDTIKYFYGLKISQVVDVDEKQNLMTTNVWLKQEWIDVKLRWNPDD 61
QY 115 YGIGKIVRPSDSVWTPDVLVFNADGRFEGT-STKTVIRYNGTVWTPPANKSSCTID 173
Db 62 YGIIHKKVPSESLWLPDVLVFNADGRFEGT-STKTVIRYNGTVWTPPANKSSCTID 121
QY 174 VTFPPFDLQNCMKFGSWTYDGSQVDIILEDQDQVDRKDFPDNGEWEIVSATGSKGNRTDS 233
Db 122 VTFPPFDLQNCMKFGSWTYDGTWVDLILINENVDKDFPDNGEWEILNAKMGKGNRDRG 181
QY 234 CCWYPTVTSFVTKRLPLFTLIIIPICIGLSFLTIVLVFVPSNEGEKICLCTSVLSLT 293
Db 182 VSYPTITVSFVLRLLPLFTLIIIPICIGLSFLTIVLVFVPSDEGEKLSLSTSVLSLT 241
QY 294 VFLVIEELIPSSSKVPIPLIGEVLTFTMIFVTLSIMVTFPAINIHRRSGSTHNAAPLVYR 353
Db 242 VFLVIEELIPSSSKVPIPLIGEVLTFTMIFVTLSIMVTFPAINIHRRSGSTHNAAPLVYR 301
QY 354 KIFLHPLKLLCMRSHVDYFT-QKEETES-----GSGPKSSRNTLEAAL 397
Db 302 RFLQKLKLLCMKDHVDYRVSSEKESQPVVKGVLEKKQKQSDGEKLVAFLEKAA 361
QY 398 NSIRYTRHIMKENDVREVVDWKFTAQVLDRLMPLFTLPSVIGSLGFLFVPIYKW 454
Db 362 DSIRYSRHVKKEHFISQVQDWFKAQVLDRIFLMLFLVSVTGSVLIPTALKW 418

RESULT 8
A33523
nicotinic acetylcholine receptor beta-3 chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 21-Jul-2000
R:Deneris, E.S.; Boulter, J.; Swanson, L.W.; Patrick, J.; Heinemann, S.
J. Biol. Chem. 264, 6268-6272, 1989
A:Title: Beta-3: a new member of nicotinic acetylcholine receptor gene family is expressed
A:Reference number: A33523; MUID:89197926; PMID:2703489

A:Accession: A33523
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-464 <DEN>
A:Cross-references: GB:J04636; NID:93298521; PIDN:AAC28887.1; PID:g205614
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor; transmembrane protein

Query Match 62.5%; Score 1534; DB 2; Length 464;
Best Local Similarity 65.1%; Pred. No. 1.9e-118;
Matches 286; Conservative 71; Mismatches 62; Indels 20; Gaps 3;

QY 33 AQRGLSEPSIIAKHEDSLKDLFQDYERWVRPVEHLNDKIKIFGLAISQVVDVDEKQNL 92
Db 24 ATAGL---SSVAEHEDALLRHLFQGYQKWRPVLNSSDIIVYFGLKISQVVDVDEKQNL 80
QY 93 MTNVLWKQEWIDVKLRWNPDDYGGIKVIRVPSDSVWTPDVLVFNADGRFEGT-STKTV 151
Db 81 MTNVLWKQEWIDVKLRWNPDDYGGIKVIRVPSDSVWTPDVLVFNADGRFEGT-STKTV 140
QY 152 IRYNGTVWTPPANKSSCTIDVTPPPDLQNCMKFGSWTYDGSQVDIILEDQDQVDRK 211
Db 141 VKSQSGTVSWTPPANKSSCTMDVTPPPDLQNCMKFGSWTYDGTWVDLILINENVDK 200
QY 212 PFDNGEWEIVSATGSKGNRTDSCWYPTVTSFVTKRLPLFTLIIIPICIGLSFLTIV 271
Db 201 PFDNGEWEILNAKMGKGNRREGFYSPFTVTSFVTKRLPLFTLIIIPICIGLSFLTIV 260
QY 272 FYLPNEGEKICLCTSVLSLTIVLVFVPSNEGEKIVPIPLIGEVLTFTMIFVTLSIMVT 331
Db 261 FYLPNEGEKLSLSTSVLSLTIVLVFVPSNEGEKIVPIPLIGEVLTFTMIFVTLSIMVT 320
QY 332 VFAINIHRRSGSTHNAAPLVYRQKIFLHPLKLLCMRSHVDY-----FT 375
Db 321 VFVINHRRSGSTHNAAPLVYRQKIFLHPLKLLCMRSHVDY-----FT 380
QY 376 QKEETESGSGPKSSRNTLEAALNSIRYTRHIMKENDVREVVDWKFTAQVLDRLMFLWTF 435
Db 381 KRKQTPASDGERVLVAFLEKASESIRYISRHVKKEHFISQVQDWFKAQVLDRIFLWLF 440
QY 436 LFVSIVGSGLGFLFVPIYKW 454
Db 441 LIASVLGSLIIPALKW 459

RESULT 9
S16333
nicotinic acetylcholine receptor non-alpha-3 chain precursor - goldfish
C:Species: Carassius auratus (goldfish)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C:Accession: S16333
R:Caulley, K.; Agranoff, B.W.; Goldman, D.
J. Neurosci. 10, 670-683, 1990
A:Title: Multiple nicotinic acetylcholine receptor genes are expressed in goldfish retina
A:Reference number: S16333; MUID:90155434; PMID:2303867
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-466 <CAU>
A:Cross-references: EMBL:M29529; NID:g212955; PIDN:AAA49167.1; PID:g212956
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor; transmembrane protein

Query Match 62.3%; Score 1531; DB 2; Length 466;
Best Local Similarity 64.8%; Pred. No. 3.4e-118;
Matches 283; Conservative 63; Mismatches 67; Indels 24; Gaps 3;

QY 42 STAKHEDSLKDLFQDYERWVRPVEHLNDKIKIFGLAISQVVDVDEKQNLMTTNVWLKQ 101
Db 27 STAKHEDTLRLNLFRCYQKWRPVLNANDITVRFGLKISQVVDVDEKQNLMTTNVWLQ 86
QY 102 EVIDVKLRWNPDDYGGIKVIRVPSDSVWTPDVLVFNADGRFEGT-STKTVIRYNGTVW 160

Db 87 EWTYKLRNPPEDYGGITSIRVPSSETIWLPDIVLYENADRGFEGLMTKAIIVRFNGTIMW 146
 Qy 161 TPPANYKSSCTIDVTFFPDQNCMKFGSWTYDGSQVDIILEDQDVKDRDFDNGWEWI 220
 Db 147 TPPASYKSSCTMDVTFFPDQNCMKFGSWTYDGTWVDLTLLDAYVDRKDFDNGWEWI 206
 Qy 221 VSATSGKGRNTDCCWYVTVTSFVVKRLPLPYTLFLIIPCLGLSFLTLVFLYPLSNRGE 280
 Db 207 LNATGQRSGRRGIYSYFVTVSFLLKRLPLPYTLFLIIPCLGLSFLTLVFLYPLSDRGE 266
 Qy 281 KICLCTSVLSLTVFLLVIEEIPSSKVIPLIGEYLVFTMIFVTLSTMVTFVAINIHR 340
 Db 267 KLLSTSVLSLTVFLLVIEEIPSSKVIPLIGEYLVFTMIFVTLSTMVTFVAINIHR 326
 Qy 341 SSSSTHNAAPLVKRIFLHTLPLKLCWRSHVDYR-----FTQKEETES 382
 Db 327 SSATYHPNAPWKSLFLQRLPRLLCWRGHTDRYQYDPDIELRSPELKGMKQKQSGAGG 386
 Qy 383 GSGPKSSN-----TLEAALNSIRYITHIMKENDVREVEDWKFAIOVLORMFLWTLF 437
 Db 387 RGGLKEDENQAWIALLEKATHSVHYISRIKHEHFIREVQDQKFAVQVLDRIFLWVFLT 446
 Qy 438 VSIVGSLGLFVPVIYKW 454
 Db 447 ASVLGTILIFTALHWY 463
 RESULT 10
 A40110
 nicotinic acetylcholine receptor alpha-2 chain precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 20-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 20-Aug-1999
 C:Accession: A40110
 R:Wada, K.; Ballivet, M.; Boulter, J.; Connolly, J.; Wada, E.; Deneris, E.S.; Swanson, I.
 Science 240, 330-334, 1998
 A:Title: Functional expression of a new pharmacological subtype of brain nicotinic acetylcholine receptor
 A:Reference number: A40110; MUID:86178113; PMID:2832952
 A:Accession: A40110
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-511 <WAD>
 A:Cross-references: GB:M20297; NID:G202672; PIDN:AAA40664.1; PID:G202674
 A>Note: the authors translated the codon TCG for residue 494 as Cys
 C:Superfamily: acetylcholine receptor
 C:Keywords: neurotransmitter receptor
 Query Match 48.2%; Score 1184; DB 2; Length 511;
 Best Local Similarity 49.2%; Pred. No. 1.5e-89;
 Matches 236; Conservative 70; Mismatches 106; Indels 68; Gaps 6;
 Qy 37 LSEPSIAKHEDSLKDLFQDYERWVRPVEHLNDKIKIFGLAISQLVDDVDEKQMLMTN 96
 Db 26 LTQGSHTHADRLFKHLFGGYNWARVPNTSDVIVRGLSLAQILDVDEKQMLMTN 85
 Qy 97 VNLQKQWIDVLRNPPDDYGGIKVIRVPSDSVTPDVLFDNADRGFEGLT-STKTVRYN 155
 Db 86 VNLQKQWIDVLRNPPDDYGGIKVIRVPSDSVTPDVLFDNADRGFEGLT-STKTVRYN 145
 Qy 156 GTVTWTPPNYKSSCTIDVTFFPDQNCMKFGSWTYDGSQVDIILEDQDVKDRDFDN 215
 Db 146 GTVHWVPPAIYKSSCSIDVTFFPDQNCMKFGSWTYDGSQVDIILEDQDVKDRDFDN 205
 Qy 216 GEWIVSATSGKGRNTDSCC--WYPVTVTSFVIRKRLPLFYTLFIIPCLGLSFLTLVIFY 273
 Db 206 GEWAIINATGYNSKKYDCCAEIPDVTVYFVIRRLPLFYTLFIIPCLGLSFLTLVIFY 265
 Qy 274 LPSNEGEKICLCTSVLSLTVFLLVIEEIPSSKVIPLIGEYLVFTMIFVTLSTMVTF 333
 Db 266 LPSECGEKITLCISVLSLTVFLLVIEEIPSSKVIPLIGEYLVFTMIFVTLSTMVTF 325
 Qy 334 AINTHRSSTHNAAPLVKRIFLHTLPLKLCMRSHV----- 370
 Db 326 VLNVHRSSTHNAAPLVKRIFLHTLPLKLCMRSHV----- 384

Qy 371 ---DRYFQKEETESGSG-----PKSSRNTL----- 393
 Db 385 MDAGERETETETETETENICVACAGLPDSSMGVLYGHGLHRLAMEPETKTPSQASEILL 444
 Qy 394 ---EALNLSIRYITHIMKENDVREVEDWKFAIOVLDRMFLWTLFVSVIGSLGLFVP 449
 Db 445 SPQIQKALEGVHYIADRLSRSDADSSVKEDWKYVAMVVDRIPLMLFIIVSVGLTGTLFLP 504
 RESULT 11
 ACCHZN
 nicotinic acetylcholine receptor alpha-2 chain precursor, neuronal - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
 C:Accession: S00377
 R:Nef, P.; Oneyser, C.; Alliod, C.; Couturier, S.; Ballivet, M.
 EMBO J. 7, 595-603, 1988
 A:Title: Genes expressed in the brain define three distinct neuronal nicotinic acetylcholine receptor subunit families
 A:Reference number: S00376; MUID:88283624; PMID:3267226
 A:Accession: S00377
 A:Molecule type: DNA
 A:Residues: 1-528 <NEP>
 A:Cross-references: EMBL:X07339; NID:G62792; PIDN:CAB59645.1; PID:G6136914
 C:Genetics:
 A:Introns: 21/1; 73/3; 88/3; 125/2; 487/3
 C:Superfamily: acetylcholine receptor
 C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane; F1-23/Domain: signal sequence #status predicted <SIG>
 F:24-528/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <MAT>
 F:241-260/Domain: transmembrane #status predicted <TM1>
 F:272-290/Domain: transmembrane #status predicted <TM2>
 F:306-327/Domain: transmembrane #status predicted <TM3>
 F:502-520/Domain: transmembrane #status predicted <TM4>
 F:54,104/Binding site: carbonyl group (Asn) (covalent) #status predicted
 F:158-172,222-223/Dissulfide bonds: #status predicted
 Query Match 47.5%; Score 1166.5; DB 1; Length 528;
 Best Local Similarity 46.9%; Pred. No. 4.3e-88;
 Matches 236; Conservative 72; Mismatches 106; Indels 89; Gaps 7;
 Qy 33 AQRLGSPSSIAKHEDSLKDLFQDYERWVRPVEHLNDKIKIFGLAISQLVDDVDEKQML 92
 Db 22 ATREKQKQHPGA--EDRLFKHLFTGYNRWSRPVNTSDVIVRGLSLAQILDVDEKQML 79
 Qy 93 MTTNVLKQWIDVLRNPPDDYGGIKVIRVPSDSVTPDVLFDNADRGFEGLT-STKTV 151
 Db 80 MTTNVLKQWIDVLRNPPDDYGGIKVIRVPSDSVTPDVLFDNADRGFEGLT-STKTV 139
 Qy 152 IRVNGTIVTTPPNYKSSCTIDVTFFPDQNCMKFGSWTYDGSQVDIILEDQDVKDR 211
 Db 140 LPSNGKVKWVPPAIYKSSCSIDVTFFPDQNCMKFGSWTYDCAKIDLENHEHVDLKD 199
 Qy 212 FPDNGEWEIVSATSGKGRNTDSCC--YPVTVTSFVIRKRLPLFYTLFIIPCLGLSFLTV 269
 Db 200 YWESGEWAIINAGRYNSKKYDCCAEIPDVTVYFVIRRLPLFYTLFIIPCLGLSFLTV 259
 Qy 270 LVFVLPSEGEKICLCTSVLSLTVFLLVIEEIPSSKVIPLIGEYLVFTMIFVTLSTM 329
 Db 260 LVFVLPSEGEKICLCTSVLSLTVFLLVIEEIPSSKVIPLIGEYLVFTMIFVTLSTM 319
 Qy 330 VTVPAINHRSSTHNAAPLVKRIFLHTLPLKLCMR----- 367
 Db 320 ITVFLNVHRSSTHNAAPLVKRIFLHTLPLKLCMR----- 378
 Qy 368 -----SHVDYFTQKEETE-----SG 383
 Db 379 STSRCLWETDVKWEEEBEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEEKEE 438
 Qy 384 SGPKSSRNTLEA-----ALNSIRYITHIMKENDVREVEDWKFAIOV 426
 Db 439 SGGPAPQVPLKGBEVSQDGLTSLPSILRALLEGVQYIADHRAEDADFSVKEDWKYVAMV 498

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 21:23:42 ; Search time 345 Seconds
(without alignments)
253.342 Million cell updates/sec

Title: US-09-703-951A-8
Perfect score: 2456
Sequence: 1 MAARGSPRALRLLLVQLV.....PVIYKWNILIPVHIGNANK 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 696363 seqs, 186758610 residues

Total number of hits satisfying chosen parameters: 696363

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2456	100.0	468	12	US-10-349-836-8
2	1586	64.6	458	12	US-10-349-836-16
3	1201.5	48.9	529	12	US-10-349-836-2
4	1169	47.6	528	10	US-09-892-985-2
5	1157.5	47.1	627	12	US-10-349-836-6
6	1135	45.2	494	12	US-10-349-836-10
7	1126.5	45.9	622	10	US-09-941-179A-3
8	1119	45.6	631	10	US-09-941-179A-7
9	1115	45.4	504	12	US-10-349-836-4
10	1102.5	44.9	502	15	US-10-157-031-92
11	1098.5	44.7	622	10	US-09-941-179A-11
12	1087	44.3	504	10	US-09-892-985-4
13	1082.5	44.1	627	10	US-09-892-985-6
14	1062.5	43.3	479	12	US-10-349-836-20
15	1028.5	41.9	498	12	US-10-349-836-18

16	1015.5	41.3	498	10	US-09-892-985-12
17	1014	41.3	457	15	US-10-157-031-28
18	1011	41.2	437	12	US-10-261-798-69
19	984	40.1	502	10	US-09-892-985-10
20	984	40.1	502	12	US-10-349-836-14
21	980	39.9	449	15	US-10-199-995-2
22	979	39.9	529	9	US-09-795-693-31
23	979	39.9	529	15	US-10-156-239-31
24	979	39.9	529	15	US-10-199-485-31
25	850.5	34.6	496	9	US-09-303-232-4
26	841.5	34.3	501	9	US-09-303-232-6
27	776.5	31.6	502	12	US-10-352-684A-56
28	774.5	31.5	502	10	US-09-892-985-8
29	770.5	31.4	502	11	US-09-954-936-2
30	762	31.0	770	9	US-09-303-232-2
31	744.5	30.3	450	9	US-09-795-693-11
32	744.5	30.3	450	15	US-10-156-239-11
33	744.5	30.3	450	15	US-10-199-485-11
34	741.5	30.2	450	12	US-10-312-088-38
35	713	29.0	520	15	US-10-012-542-144
36	694	28.3	554	12	US-10-203-968-12
37	576	23.5	210	9	US-09-820-339A-2
38	562	22.9	479	12	US-10-203-968-11
39	553.5	22.5	235	9	US-09-820-339A-6
40	551	22.4	635	12	US-10-203-968-10
41	538.5	21.9	230	9	US-09-820-339A-8
42	479.5	19.5	446	12	US-10-349-836-12
43	398.5	16.2	441	9	US-09-732-680A-2
44	397	16.2	132	11	US-09-899-495-86
45	389.5	15.9	457	12	US-10-243-475-132

ALIGNMENTS

RESULT 1

US-10-349-836-8
; Sequence 8, Application US/10349836
; Publication No. US20030138911A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,836
; FILING DATE: 23-Jan-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 07-Jun-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062

```

;
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-349-836-8

Query Match 100.0%; Score 2456; DB 12; Length 468;
Best Local Similarity 100.0%; Pred. No. 3.4e-233;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAARGSPRALRLLLVQLVAGRCGLAGAGGAGQGLSEPSIAKHEDSLKDLFQDYER 60
DB 1 MAARGSPRALRLLLVQLVAGRCGLAGAGGAGQGLSEPSIAKHEDSLKDLFQDYER 60
QY 61 WVRPVEHLNDKIKIKFGLAISQLVDVDEKQMLTNNVWLKQEWIDVKLRWNPDDYGGIKV 120
DB 61 WVRPVEHLNDKIKIKFGLAISQLVDVDEKQMLTNNVWLKQEWIDVKLRWNPDDYGGIKV 120
QY 121 IRVPSDSVWTPDVLVFNADGRFGTSTKTVIRYNGVTWTPPNYKSSCTIDVTREPPD 180
DB 121 IRVPSDSVWTPDVLVFNADGRFGTSTKTVIRYNGVTWTPPNYKSSCTIDVTREPPD 180
QY 181 LQNCMKFGSWTVDGSDVDIILEDQVDKRDFFDNGEWEIVSATSGKGNRTDSCCYPYV 240
DB 181 LQNCMKFGSWTVDGSDVDIILEDQVDKRDFFDNGEWEIVSATSGKGNRTDSCCYPYV 240
QY 241 TYSFVIRKRLPFTFLIIPICIGLSFLTIVLVFVLPSEGEKICICTSVLSVLTFLVIE 300
DB 241 TYSFVIRKRLPFTFLIIPICIGLSFLTIVLVFVLPSEGEKICICTSVLSVLTFLVIE 300
QY 301 EIIPSSSKVPLIGEYLVFTMIFTVLSIMVTVPAINTHRSSSTHNAWAPLVKIFLHTL 360
DB 301 EIIPSSSKVPLIGEYLVFTMIFTVLSIMVTVPAINTHRSSSTHNAWAPLVKIFLHTL 360
QY 361 PKLLCMRSHVDVRYFTQKEETESGPKSSRNTLEAALNSIRYITRHKMKENDVREVVEDW 420
DB 361 PKLLCMRSHVDVRYFTQKEETESGPKSSRNTLEAALNSIRYITRHKMKENDVREVVEDW 420
QY 421 KFTAQVLDRLMFLWTFVSVIGSLGLFPVPIYKWNILIPVHIGNANK 468
DB 421 KFTAQVLDRLMFLWTFVSVIGSLGLFPVPIYKWNILIPVHIGNANK 468

RESULT 2
US-10-349-836-16
; Sequence 16, Application US/10349836
; Publication No. US20030138911A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; ADDRESS: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

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;
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,836
; FILING DATE: 23-Jan-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 07-Jun-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-349-836-16

Query Match 64.6%; Score 1586; DB 12; Length 458;
Best Local Similarity 65.8%; Pred. No. 1.9e-147;
Matches 302; Conservative 63; Mismatches 66; Indels 28; Gaps 5;

QY 13 LLLVLQVLVAGRCGLAGAGGAGQGLSEPSIAKHEDSLKDLFQDYERWVRPVEHLNDKI 72
DB 6 MLVLVL-----GIPSSATGTF--NSIAENEDALLRHLFGQYKQWVRPVLHNSDTI 54
QY 73 KIKFGLAISQLVDVDEKQMLTNNVWLKQEWIDVKLRWNPDDYGGIKVIRVPSDSVWTPD 132
DB 55 KYVFGGLKISQLVDVDEKQMLTNNVWLKQEWIDVKLRWNPDDYGGIHSIKVPSESLWLPD 114
QY 133 IVLFDNADGRFECT-STKTVIRYNGVTWTPPNYKSSCTIDVTFFPFDLQNCMKFGSW 191
DB 115 IVLFDNADGRFEGSLTKVIVKNGVTWTPPNYKSSCTMDVTFFPFDQNCMKFGSW 174
QY 192 TYDGSQVDIILEDQVDKRDFFDNGEWEIVSATSGKGNRTDSCCYPYVTVYSFVIRKRLPL 251
DB 175 TYDGTWVDLILINENVDRKDPFDNGEWEILNAGKMGNNRDRGVYSYFFITYSFVLRRLPL 234
QY 252 FYTLPLIIPICIGLSFLTIVLVFVLPSEGEKICICTSVLSVLTFLVIEIIPSSSKVIP 311
DB 235 FYTLPLIIPICIGLSFLTIVLVFVLPSEGEKICICTSVLSVLTFLVIEIIPSSSKVIP 294
QY 312 LIGELYLVFTMIFTVLSIMVTVPAINTHRSSSTHNAWAPLVKIFLHTLKLKCMRSHVD 371
DB 295 LIGELYLVFTMIFTVLSIMVTVPAINTHRSSSTHNAWAPLVKIFLHTLKLKCMRSHVD 354
QY 372 RYFT-QKEETES-----GSGPKSSRNTLEAALNSIRYITRHKMKENDVRE 415
DB 355 RYSSPEKEESQPVVKGKVKLKKQKQLSDGEKLVAFLEKAADSIRYISRHVKKEHFIQ 414
QY 416 VVEDWKFIAQVLDRLMFLWTFVSVIGSLGLFPVPIYKWN 454
DB 415 VVQDWKFAQVLDRLMFLWTFVSVIGSLGLFPVPIYKWN 453

RESULT 3
US-10-349-836-2
; Sequence 2, Application US/10349836
; Publication No. US20030138911A1

```

GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/349,836
FILING DATE: 23-Jan-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
APPLICATION NUMBER: 08/484,722
FILING DATE: 07-Jun-95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-349-836-2
Query Match 48.9%; Score 1201.5; DB 12; Length 529;
Best Local Similarity 50.5%; Pred. No. 1.9e-109;
Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;
37 LSEPSIA-----KHEDSLKDLFDYERWRVPEHLNDKIKIKFGLAISQLVDVE 88
41 LSSPSPTALPOGSGSTETEDRLFHPRGNRWRPVNTSDVIVRFLGSLAQILDVDE 100
89 KNQLMTNVLKQEWIDVKLRNPDYGGIKVIRVPSDVTPDVLFDNADRGEGT-S 147
101 KNQMTTNVLKQESDVKLRNPDGNTSLRVPSEMIWPDIVLYNNADGEFATVM 160
148 TKTVIRYNGVTWTPPNYKSCITDVTFFFDLQNCMKFGSWTYDGSQVDIILEDQDV 207
161 TKALFSTGTVHVHPVPAIKSSCSIDVTFFFDQNCCKFGSWTYDKAKIDLEQMEQTV 220
208 DKRFFDNGEWEIVSATSGKNRTDSCC--WYPVYTVSFVIRKPLFLFTFLIIPCIGLS 265
221 DLKDYWESGEAIVNATGYNKDYCCAEIYPDVTYAFVIRRLPLFTVINLIIPCLLIS 280
266 FLTVLVFLVPSNEGEKICLCTSVLSVLTFLVLLVIEEIIIPSSKVIPLIGEVLVFTMIPVT 325
281 CLTVLVFLVPSDCGEKICLCTSVLSVLTFLVLLVIEEIIIPSSKVIPLIGEVLVFTMIPVT 340

326 LSIWTVFPAINHRRSSSTNNAPLVKRIKIFLHTLPKLLCM----- 366
341 LSIWTVFVLNVHRRSPSTH-TMPHWVRGALLGCVPRWLLMNRPPVPVLCPLRLKLSLP 399
367 -----RSHPD---RYFTQKGET-----ESGSGPKSS----- 389
400 SYHWLESNVDAEREVVVEEDRWACAGHAPSVGTLCSHGHLHSGASGPKAEALLQGE 459
390 ---RNTLEAALNSIRYITRHKENDVREVVEDWKFIAQVLDRLMFLWTFLEVSIVGSLG 446
460 LLLSPHMQKALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDRIFLMLFIIVCFGLTGL 519
447 FVP 449
520 FLP 522
RESULT 4
US-09-892-985-2
; Sequence 2, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; Ellis, Steven B.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 528 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-892-985-2
Query Match 47.6%; Score 1169; DB 10; Length 528;
Best Local Similarity 49.9%; Pred. No. 3e-106;
Matches 241; Conservative 65; Mismatches 105; Indels 72; Gaps 9;

; Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/349,836
 ; FILING DATE: 23-Jan-2003
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/660,451A
 ; FILING DATE: June 7, 1996
 ; APPLICATION NUMBER: 08/484,722
 ; FILING DATE: 07-Jun-95
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-9370B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-238-0999
 ; TELEFAX: 619-238-0062
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 494 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-10-349-836-10

Query Match 46.2%; Score 1135; DB 12; Length 494;
 Best Local Similarity 46.1%; Pred. No. 6.2e-103;
 Matches 218; Conservative 89; Mismatches 102; Indels 64; Gaps 7;
 QY 47 EDSLKLLKDLFQDYERWVRVEHLNDKIKIKFGLAISQVLDVDEKNOIMTNVWLKQEWIDV 106
 Db 34 EERLFKLFHSYQIRPVENVSDPTVHFVAITQLANVDVDMQIMETNLRLHINDY 93
 QY 107 KLRNMPDDYGGIKVIRVPSDSVWTPDIVLFONADGRF--EGTSTKTVIRYNGTWTTPPA 164
 Db 94 KLRWDPMEYDGIETLRVPADKIWKEDIVLYNNAVGFQVEG-KTKALLKNGMITWTPPA 152
 QY 165 NYKSSCTIDVTFFPDLQNCMKFGSWTYDGSQVDIILEDQVDKDFDNGEWEIVSAT 224
 Db 153 IFKSSCPMDITFPFPPDHQCSLKFGSWTYDKAEIDLIIAGSKVDNMDFWENSEWEIIDAS 212
 QY 225 GSKGNRTDSCC--WYPVVTYSFVIKELPLFYTLFLIIPCIGLSFLTIVFLVPSNEGEKI 282
 Db 213 GYKHDIKNCCBEITDITFYIRRLPMFYTNLIIPCILFSFTVFLVFLPSCGSKV 272
 QY 283 CLCTSVLSLVTLVFLVIEEIIIPSSSKVPIPLIGEYLVFTMI FVTLSIMVTVFAINIHRS 342
 Db 273 TLICISVLSLVTLVFLVITETIPSTSLVPLVGEYLLFTMI FVTLSIVTVFVLNIHYRTP 332
 QY 343 STHNAMAPLVKIFLHTLPLKLCMRSHVDH-----GPKSSRN-----TLEALNSIR 401

Db 333 TTH-TMPRWKTVFLKLLPQVLLMRWPLDKTRGTGSDAVPRGLARRPAKGLASHGEPRH 391
 QY 373 ----YFTQKEETESGSGPKSSRNTL-----EALNSIRYITRHMKNKDVRE 415
 Db 392 LKECFHCKHSNELATSKERLSHQPLQWVENSEHSEPEVDVINSVQFIAENKMSHNETKE 451
 QY 416 VVEDWKFTAQVLDRLMFLMTFLFVSI VSGLSGLFVPVVIYKWANLILPVHIGNANK 468
 Db 452 VEDDKWYVAMVVDVRFVFLWVFIVCVFGTAGLFLQPL-----LGNTGK 493

RESULT 7

US-09-941-179A-3
 ; Sequence 3, Application US/09941179A
 ; Patent No. US20020146765A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Aktiengesellschaft
 ; TITLE OF INVENTION: Acetylcholine receptor subunits
 ; FILE REFERENCE: Le A 34 821
 ; CURRENT APPLICATION NUMBER: US/09/941,179A
 ; CURRENT FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: DE 100 42 177.6
 ; PRIOR FILING DATE: 2000-08-28
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 622
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
 ; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
 ; OTHER INFORMATION: receptor
 US-09-941-179A-3

Query Match 45.9%; Score 1126.5; DB 10; Length 622;
 Best Local Similarity 38.9%; Pred. No. 6e-102;
 Matches 229; Conservative 78; Mismatches 98; Indels 183; Gaps 7;
 QY 44 AKHEDSLKLLKDLFQDYERWVRVEHLNDKIKIKFGLAISQVLDVDEKNOIMTNVWLKQEW 103
 Db 29 AHABERLLKLLKDLFQDYERWVRVEHLNDKIKIKFGLAISQVLDVDEKNOIMTNVWLKQEW 88
 QY 104 IDVKLRNMPDDYGGIKVIRVPSDSVWTPDIVLFONADGRFECT-STKTVIRYNGTWTTP 162
 Db 89 HDYKLRWDPQYENVTSIRIPSELIRWDPDIVLYNNAVGFVTLKATLNTYGRVWRP 148
 QY 163 PANYKSSCTIDVTFFPDLQNCMKFGSWTYDGSQVDIILEDQVDKDFDNGEWEIVS 222
 Db 149 PAIYKSSCEIDVEYFPFDPQTCVMKFGSWTYDKAKIDLVSMSHSHVDQDLYWESGEWIIIN 208
 QY 223 ATGSKGNRTDSCC--WYPVVTYSFVIKELPLFYTLFLIIPCIGLSFLTIVFLVPSNEGE 280
 Db 209 AVGNYSKKYECCTEYIPDITYSPIIRRLPYFTINLIIPCILISCLTIVFLVFLPSECGE 268
 QY 281 KICLCTSVLSLVTLVFLVIEEIIIPSSSKVPIPLIGEYLVFTMI FVTLSIMVTVFAINIHHR 340
 Db 269 KITLCISVLSLVTLVFLVITETIPSTSLVPLVGEYLLFTMI FVTLSIIITVFLVNVHR 328
 QY 341 SSSTHNAMAPLVKIFLHTLPLKLCMR-----SHVD----- 367
 Db 329 SPRTH-TMPDWRRVRFIDVPRLLFMKRPSTVKONCKKLIESMHKLITNSPRLWSETDMEP 387
 QY 368 -----SHVD----- 371
 Db 388 NFTSSSPSPQSNBPSPTSSFAHLEBPAPKPMCKSPGQYSMLHPPEPQVTCSSPKPSCH 447
 QY 372 -----RYFTQKEETESG----- 384
 Db 448 PLSDTOTTSISKGRSLSVQOQMYSPNKTEEGSIRCSRISIQCYLOEDSSQTNHGSSASPA 507
 QY 385 -----GPKSSRN-----TLEALNSIR 401

Db 508 SQRCHLNEBQPHKPHOCKKCRKGEAAGTPTQGSKSHNKGHEHLVLMSPALKLAVEGVH 567
 Qy 402 YITRHKMKENDVRVVEDWKPIAQVLDRMFLLWTFLFVSIVGSLGLFVP 449
 Db 568 YIADHLRAEDAFSVKEDWKYVANVIDRIFLMMFIIVCLLGTVGLFLP 615
 RESULT 8
 US-09-941-179A-7
 ; Sequence 7, Application US/09941179A
 ; Patent No. US20020146765A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Aktiengesellschaft
 ; TITLE OF INVENTION: Acetylcholine receptor subunits
 ; FILE REFERENCE: Le A 34 821
 ; CURRENT APPLICATION NUMBER: US/09/941.179A
 ; CURRENT FILING DATE: 2001-08-27
 ; PRIOR APPLICATION NUMBER: DE 100 42 177.6
 ; PRIOR FILING DATE: 2000-08-28
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 631
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
 ; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
 ; OTHER INFORMATION: receptor
 US-09-941-179A-7
 Query Match 45.6%; Score 1119; DB 10; Length 631;
 Best Local Similarity 38.5%; Pred. No. 3.3e-101;
 Matches 230; Conservative 81; Mismatches 94; Indels 192; Gaps 8
 Qy 44 AKHEDSLKOLFQDYERWRPVEHLNKKIKIKFGLAISQLVDVERKNQMTTNVWLKQEW 103
 Db 29 AHAEERLLKFLSGYNKWSRPVANISDVLVRFGLSIAQLIDVDEKKNQMTTNVWLKQEW 88
 Qy 104 IDVKLRNPDYGGIKIVRPDSVTPWDIVLFONADGREGTS-TKTVIRYNGTVTWTP 162
 Db 89 HDVKLRWDPOEYENVTISIRPSELIWRPDIIVLYNNADGFVATHLTKAHLFYDGRKWWP 148
 Qy 163 PANYKSSCTIDVTFPPFDLQNCMKFGSWTDGSOVDII-----LEPDQVDKRDFF 213
 Db 149 PAIYKSSCSIDVTFPPDQNCMKFGSWTDKAKIDLVSMSHSGRTNVVELGVDOLDYW 208
 Qy 214 DNGEWETVSATGSKGNRTDSCW--YPVTVYSFVIKRLPLFYTLFIIPCTIGLSEPLTVLV 271
 Db 209 ESGEWVINA VGNVNSKYECCTEIIYPDITYSFIIIRLPLEFVTLNLIIPCLLSICLTVLV 268
 Qy 272 FYLPSNGEKICLCTSLVLSVTFLLVTEBIIIPSSKVIPLIGEVLVTFMIFVTLINMVT 331
 Db 269 FYLPSECGEKITLCISLLSVTFLLLTETIIPSTSLVIPLIGEYLLFTMIFVTLISIIIT 328
 Qy 332 VFAINIHRSSSTHNAMAPLVKRIFLHLPKLLCWR-----SHVD----- 367
 Db 329 VFVLNVHRSPRTH-TWPDWVRVFLDIVPRLLFMKRPSTVKDNCCKLIESMHKLTNSPR 387
 Qy 368 -----SHVD----- 371
 Db 388 LWSETDMEPNPTTSSPSQSNESPTSSFCALHEEPAPKWCPSGOYSMLHPEPPQVT 447
 Qy 372 -----RYFTQKETESGS----- 384
 Db 448 CSGPKPSCHPLSDQTTSISKGRSLSVQOMYSPNKTEEGSIRCRSRSIQCYCLOEDSSQT 507
 Qy 385 -----GPKSSRN-----T 392
 Db 508 NGHSSASPASORCHLNEBQPHOCKKCRKGEAAGTPTQGSKSHNKGHEHLVLMSPA 567
 Qy 393 LEAALNSIRYITRHKMKENDVRVVEDWKPIAQVLDRMFLLWTFLFVSIVGSLGLFVP 449

Db 165 FFFDYQNTMFGWSYDKAKIDLVLIGSSWNLKDYWESGEWAIKAPGYKHDIKYNCE 224
Qy 236 -WYPVYTSFVVKRLPLFYTLFIIPICIGLSFLTVLFLVPSNEGEKICLCTSVLVSITV 294
Db 225 EYDPDITVSLVIRRLPLFYTLFIIPICLLISFLTVLFLVPSDCGEKVTLCISVLSITV 284
Qy 295 FLLVIEEIPSSKVIPIGLGYLFTMTFVLSIMVTVPAINIHRSSSTTNAMAPLVRK 354
Db 285 FLLVITETIPSTSLVPIGLGYLFTMTFVLSIVITVFLNVHRYTPTTH-TWPSWVKT 343
Qy 355 IFLHLPKLLCMR----- 367
Db 344 VFLNLLPRVMTPTSGNEGNAQPRPLYGAELSNLNCFSRAESKGCKEGYPCQDGMCGY 403
Qy 368 -----SHVDYFTQKEETESGPKS-----SRNTLEAALNSIRYITRHHMKENDVREV 416
Db 404 CHHRRIKISNFSANLTRSSSESVDVLSALSALPEIKATQSVKYIAENKMAQNEAKEI 463
Qy 417 VEDWKFAIQVLDRLMFLWTLFVLSVIGSLGFV 448
Db 464 QDDWKYVAMVIDRIFLWVTLVLCILGTAGLEL 495

RESULT 10
US-10-157-031-92
; Sequence 92, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-92

Query Match 44.9%; Score 1102.5; DB 15; Length 502;
Best Local Similarity 43.2%; Pred. No. 1e-99;
Matches 220; Conservative 93; Mismatches 119; Indels 77; Gaps 6;
Qy 1 MAARGSPRALRLLLLVLAGRCGLAGAGGAQGLSEPPSSIAKHEDSLKDLFQDYER 60
Db 1 MALAVSLPLACRALLULLLS-----LLPVARASEAERHLEFEDYNE 45
Qy 61 WRPVEHLNDKIKIFGLAISQVVDVEKQMLTNNVWLKQEWIDVLRWNPDDYGGIKV 120
Db 46 IIREVANVSDPVIIHFEVMSQLVKVDENVQIMETNLWLKQIWNKYDKWNPSPGYGAEF 105
Qy 121 IRVPSDSVWTPDVLFDNADGRFE-GTSTKTVIYNGTVTTPPANKSSCTIDVTPFP 179
Db 106 MRVPAQKWKRPDIIVLYNNAVGDFOVTKTKALLKYTGVTWIPPAIFKSSCKIDVTPFP 165
Qy 180 DLQCSMKFGSWTYDGSQVDIILEDQVDKDFPDNGEWEIVSATSGKGNRTDSCC--WY 237
Db 166 DYQNTWKFGWSYDKAKIDLVLIGSSWNLKDYWESGEWAIKAPGYKHDIKYNCEIY 225
Qy 238 PYVYTSFVVKRLPLFYTLFIIPICIGLSFLTVLFLVPSNEGEKICLCTSVLVSITV 297
Db 226 PDITYSLYSRRLPLFYTLFIIPICLLISFLTVLFLVPSDCGEKVTLCISVLSITV 285
Qy 298 VIEEIPSSKVIPIGLGYLFTMTFVLSIMVTVPAINIHRSSSTTNAMAPLVRKIFL 357
Db 286 VITETIPSTSLVPIGLGYLFTMTFVLSIVITVFLNVHRYTPTTH-TWPSWVKT 344

Qy 358 HTLPKLLCMR----- 367
Db 345 NLLPRVMTPTSGNEGNAQPRPLYGAELSNLNCFSRAESKGCKEGYPCQDGMCGYCHH 404
Qy 368 -----SHVDYFTQKEETESGPKS-----SRNTLEAALNSIRYITRHHMKENDVREV 419
Db 405 RRIKISNFSANLTRSSSESVDVLSALSALPEIKATQSVKYIAENKMAQNEAKEI 464
Qy 420 WKFAIQVLDRLMFLWTLFVLSVIGSLGFV 448
Db 465 WKYVAMVIDRIFLWVTLVLCILGTAGLEL 493

RESULT 11
US-09-941-179A-11
; Sequence 11, Application US/09941179A
; Patent No. US20020146765A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Acetylcholine receptor subunits
; FILE REFERENCE: Le A 34 821
; CURRENT APPLICATION NUMBER: US/09/941.179A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: DE 100 42 177.6
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Modified alpha
; OTHER INFORMATION: 4 subunit of the chicken nicotinic acetylcholine
; OTHER INFORMATION: receptor
US-09-941-179A-11

Query Match 44.7%; Score 1098.5; DB 10; Length 622;
Best Local Similarity 38.3%; Pred. No. 3.4e-99;
Matches 225; Conservative 79; Mismatches 101; Indels 183; Gaps 7;
Qy 44 AKHEDSLKDLFQDYERWVRPVEHLNDKIKIFGLAISQVVDVEKQMLTNNVWLKQEW 103
Db 29 AHAEERLLKKLFSGYNKWSRPVANISDWLVRFLGSLAQILDVDEKQMMTTNVWKQEW 88
Qy 104 IDVKLRNPDYGGIKVIRVPSDSVWTPDVLFDNADGRPEGTS-TKTVIRYNGTVTTP 162
Db 89 HDYKLRWDPOEYENVTISIRIPSELIRPDIIVLYNADGDFAVTHLTKAHLFYDGRK 148
Qy 163 PANKSSCTIDVTPFPDQNCMKFGSWTYDGSQVDIILEDQVDKDFPDNGEWEIVS 222
Db 149 PAIYKSSCSIDVTPFPDQNCMKFGSWTYDRAKIDLVSMHSHVDLSEFVTSVENDILE 208
Qy 223 ATGSKGNRTDCCWYPY--VTYGFVIRKRLPLFYTLFIIPICIGLSFLTVLFLVPSNEGE 280
Db 209 VPAVRNEKFTCCDEPYLDITENFIIRRLPLFYTLFIIPICLLISCLTVLFLVPSCEGE 268
Qy 281 KICLCTSVLVSITVFLVIEEIPSSKVIPIGLGYLFTMTFVLSIMVTVPAINIHR 340
Db 269 KITLCISVLSITVFLVLLITETIIPSTSLVPIGLGYLFTMTFVLSIIITVFLNVH 328
Qy 341 SSSTHNAAPLVRKIIFLHLPKLLCMR----- 367
Db 329 SPRTH-TMPDWRVRFVDIVPRLLFMKRPSTVKDNCKKLESMMKLTNSPRLNSETDMEP 387
Qy 368 -----SHVD----- 371
Db 388 NFTTSSSPSQSNEPSTSSFCAHLEBPAPKPMCKSPSGQYSMLHPEPQVTCSSPKPSCH 447
Qy 372 -----RYFTQKEETESG----- 384
Db 448 PLSDTQTTSISKGRSLSVQOQMYSPNKTEGSIKRCRSRSIQCYLQEDSSQTNHSSASPA 507

QY 385 -----GPKSSRN-----TLAALNSIR 401
DB 508 SQCHLINEPOHPKQCKCKRGAAGTPTGSKSHKNGEHLVLMSPALKLAVEGVH 567
QY 402 YITRHKENDREVEDMKFIAQVLDRLMFLWTFVSVISGLFLVP 449
DB 568 YIADHLRAEDADFSVKEDWKYVAMVIDRIFLWMFIICLLGTGVLFLP 615

RESULT 12
US-09-892-985-4
; Sequence 4, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Ellis, Steven B.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-892-985-4

Query Match 44.3%; Score 1087; DB 10; Length 504;
Best Local Similarity 42.4%; Pred. No. 3.4e-98;
Matches 217; Conservative 94; Mismatches 115; Indels 86; Gaps 8;

QY 5 GSGPRAL-----RLLLVQLVAGRCGLAGAGGAGLSESPSSAKHEDSLKDLQD 57
DB 2 GSGFLSLPLALSPPRLLLL-----LSLTPVARASEAHRFLERLFD 44
QY 58 YERWVRPVEHLNDKIKFKGLAISQLVDVDEKQLMTTNVWLKQEWIDVLRWNPDDYGG 117

DB 45 YNEIIRPVANSDPVIHFVMSQVLKVDEVNQIMETNLWLKQIWXDYKLKNPDSYGG 104
QY 118 IKVIRVPSDSVMTDVLFDNADGRFE-GTSTKTVIRYNGTWTWTPPANYKSSCTIDVTF 176
DB 105 AEFMRVPAQKIWKPDVLVYNNVAVGDFQDDKTKALKKYTGVTWIPPAIFKSSCKIDVTY 164
QY 177 FFPDLQNCMKFGSWTYDGSQVDIIILEDQDVDRKDFDNGEWBIVSATGSKGNRTDSCC- 235
DB 165 FFPDYQNCMTKFGWSYDKAKIDLVLGSSMNLKDYWESGEWAIKAPGVNHDIKYNCC 224
QY 236 -WYPVYTVSFVIRKRLPLFYTLFLIIPICIGLSFLTVLVFLPSNEGSKICLCTSVLSLTV 294
DB 225 EIVPDITYSLIIRLSLFYTIILIIIPWLAIISFTIVVVFVLPSCGCKVTLICISVLSLTV 284
QY 295 FLIVIEEIIIPSSKVIPLIGEVLFTWIFVTLISIMVTVFAINIHRSSSTHNAAPLVK 354
DB 285 FLIVITETIPSTSLVPLIGVLLFTWIFVTLISIAITVFLNVHYRTPTH-TWPSVWKT 343
QY 355 IFLLHTLPKLLCMRSHVD-----RYFQKEETESGSG----- 385
DB 344 VFLNLLPRVMEWTRPTSNENNAQKPRPLYGAELSNLNCFSRAESXGCKEGYPCQDGMCGY 403
QY 386 -----PKSSRNTLEA-----ALNSIRVITRHKENDVREV 416
DB 404 CHHRIKISNFSANLTRSSSESVDVLSLSALSPEIKAEIQSVKYIAENMKQAQNEAKEI 463
QY 417 VEDWKEIAQVLDRLMFLWTFVSVISGLFLV 448
DB 464 QDDWKYVAMVIDRIFLWVFTLVCTLTGTLGL 495

RESULT 13
US-09-892-985-6
; Sequence 6, Application US/09892985
; Patent No. US20020111463A1
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; Harpold, Michael M.
; Ellis, Steven B.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-892-985-4

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CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/349,836
FILING DATE: 23-Jan-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
APPLICATION NUMBER: 08/484,722
FILING DATE: 07-Jun-95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-349-836-20

Query Match      43.3%; Score 1062.5; DB 12; Length 479;
Best Local Similarity 44.2%; Pred. No. 8.3e-96;
Matches 209; Conservative 86; Mismatches 99; Indels 79; Gaps 8;

QY   47 EDSLLKLDQDYERWRVVEHLNDKIKIFGLAISQLVDVDEKNQLMTTNVLKQEWID 106
DB   34 EERLFKLHSYNQFIIRPVENSDPTVVHFVAITQLANV-----IWN DY 78

QY   107 KLRNPPDDYGKIVRVPDSVWTPDIVLFDNADGRF--EGTSTKTIVRYNGTWTTPPA 164
DB   79 KLRLDPMEDGIEFLRAVPADKIWKPDIVLYNNAVGDFOVEG-KTKALLKYNGMITWTPPA 137

QY   165 NYKSSCTIDVTFFPDLQNCMKFGSWTYGGSOVDIILEDQDVDRDPDFDNGSWEIVSAT 224
DB   138 IFKSSCPMDITFPFPHQNCSLKFGSWTYDKAEIDLIIIGSKVKDMDFWENSEWEIIDAS 197

QY   225 GSKGNRTDSC--WYPYVTVSYFKELPLPYTLFLIIPICIGLSFLTVLVFLPSNEGEKI 282
DB   198 GYKHDIKYNCCEBEIYTDITYFYRIKLPMFYTNLIIPCLFISFLTVLVFLPSDCGEKV 257

QY   283 CLCTSIVLSLTVFLLVIEEIISSSKSVILICEYLVTMI FVTLSIMVTFAINIHRRSS 342
DB   258 TLCSIVLSLTVFLLVITITIPSTSLVPLVGEYLLFTMI FVTLSIVTVFVINHYRTP 317

QY   343 STHNAMAPLVRFKIFLHTLPKLLCMRSHVR----- 372
DB   318 TTH-TMPRWKTVFLKLLPQVLLMRPLDKTRGTSDAVPRGLARRPAKGLASHGEPRH 376

QY   373 ----YFTQKEETESGCGPKSSRNLT-----EALNSIRIYITHINKENDVRE 415
DB   377 LXECHFHCKSNELATSKRSLSHQPLQWVYVNSEHSPVEDVINSVGFI AENMKMSHNETKE 436

QY   416 VVEDWKFEIAOVLDRMFMTFLFVSIVGSGLGFVPVTVYKWNATILI PVHIGNANK 468

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Db 437 VEDDKYVAMVVRVFLWVEIIVCVFCTAGLEQL-----LGNTGK 478

RESULT 15
US-10-349-836-18
; Sequence 18, Application US/10349836
; Publication No. US20030138911A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,836
; FILING DATE: 23-Jan-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 07-Jun-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 498 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-349-836-18

Query Match 41.9%; Score 1028.5; DB 12; Length 498;
Best Local Similarity 41.5%; Pred. No. 2e-92;
Matches 207; Conservative 91; Mismatches 126; Indels 75; Gaps 11;
QY 10 ALRLLLVQLVA-GRCGLAGAGGAQRGLSEPSIAKHEDSLKDLFQD--YERWVRPVE 66
Db 6 SLVLFVLCGRGNCVANA-----EKLMDLLNKTNNLRPAT 48
QY 67 HLNDKIKIFGLAISQLVDVDEKQLMTTNVLKQEWIDVKLRNPDYGGIKIRVPSD 126
Db 49 SSSQLISIKLQLSLAQLISVNEREQIMTTNVLKQEWTDVRLTNSSRYEGVNLIRIPAK 108
QY 127 SVWTPDIVLFDNADGRE-GTSYKTVIRYNGTWTTPPANYKSSCTIDVTFPPDLQNC 185
Db 109 RIWLPDIVLYNADGTVEVSYNLIIVRSNGSVLWLPPIAYKSAKIEVKYFPFDDQNC 168

Search completed: December 23, 2003, 22:01:02
Job time : 349 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 21:19:52 ; Search time 29 Seconds
(without alignments)
682.810 Million cell updates/sec

Title: US-09-703-951A-8
Perfect score: 2456
Sequence: 1 MAARGSPRALRLLLVQLV.....PVIYKANILIPVHGNANK 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pdp:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pdp:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pdp:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pdp:*
5: /cgn2_6/ptodata/2/iaa/PTJUS_COMB.pdp:*
6: /cgn2_6/ptodata/2/iaa/backfiles.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2456	100.0	468	US-08-487-596-8	Sequence 8, Appli
2	2456	100.0	468	US-08-660-451A-8	Sequence 8, Appli
3	1586	64.6	458	US-08-660-451A-16	Sequence 16, Appl
4	1582	64.4	458	US-08-487-596-16	Sequence 16, Appl
5	1582	64.4	458	US-08-484-722-4	Sequence 4, Appli
6	1201.5	48.9	529	US-08-496-855A-2	Sequence 2, Appli
7	1201.5	48.9	529	US-08-487-596-2	Sequence 2, Appli
8	1201.5	48.9	529	US-08-660-451A-2	Sequence 2, Appli
9	1179	48.0	511	US-08-464-258B-4	Sequence 4, Appli
10	1169	47.6	528	US-08-466-589-2	Sequence 2, Appli
11	1169	47.6	528	US-08-700-636-2	Sequence 2, Appli
12	1169	47.6	528	US-08-467-574-2	Sequence 2, Appli
13	1169	47.6	528	US-09-217-345-2	Sequence 2, Appli
14	1168.5	47.6	510	US-08-278-635B-4	Sequence 4, Appli
15	1168.5	47.6	510	US-08-471-961-4	Sequence 4, Appli
16	1157.5	47.1	627	US-08-660-451A-6	Sequence 6, Appli
17	1137	46.3	629	US-08-464-258B-6	Sequence 6, Appli
18	1135	46.2	494	US-08-487-596-10	Sequence 10, Appl
19	1135	46.2	494	US-08-484-722-2	Sequence 2, Appli
20	1135	46.2	494	US-08-660-451A-10	Sequence 2, Appli
21	1132	46.1	629	US-08-278-635B-6	Sequence 10, Appl
22	1132	46.1	629	US-08-471-961-6	Sequence 6, Appli
23	1132	46.1	629	US-08-487-596-6	Sequence 6, Appli
24	1108.5	45.4	504	US-08-660-451A-4	Sequence 4, Appli
25	1093.5	44.5	497	US-08-487-596-6	Sequence 6, Appli
26	1093.5	44.5	497	US-08-278-635B-5	Sequence 5, Appli
27	1093.5	44.5	497	US-08-464-258B-5	Sequence 5, Appli

28	1087	44.3	504	2	US-08-466-589-4	Sequence 4, Appli
29	1087	44.3	504	2	US-08-700-636-4	Sequence 4, Appli
30	1087	44.3	504	3	US-08-467-574-4	Sequence 4, Appli
31	1087	44.3	504	4	US-09-217-345-4	Sequence 4, Appli
32	1082.5	44.1	627	2	US-08-466-589-6	Sequence 6, Appli
33	1082.5	44.1	627	2	US-08-700-636-6	Sequence 6, Appli
34	1082.5	44.1	627	3	US-08-467-574-6	Sequence 6, Appli
35	1082.5	44.1	627	3	US-09-217-345-6	Sequence 6, Appli
36	1062.5	43.3	479	4	US-08-660-451A-20	Sequence 20, Appli
37	1050	42.8	504	4	US-08-487-596-4	Sequence 4, Appli
38	1028.5	41.9	498	4	US-08-487-596-18	Sequence 18, Appl
39	1028.5	41.9	498	4	US-08-660-451A-18	Sequence 18, Appl
40	1016.5	41.4	457	1	US-08-278-635B-3	Sequence 3, Appli
41	1016.5	41.4	457	3	US-08-471-961-3	Sequence 3, Appli
42	1016	41.4	458	3	US-08-464-258B-3	Sequence 3, Appli
43	1015.5	41.3	498	1	US-08-496-855A-6	Sequence 6, Appli
44	1015.5	41.3	498	2	US-08-466-589-12	Sequence 12, Appl
45	1015.5	41.3	498	2	US-08-700-636-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-487-596-8
; Sequence 8, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062

```
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-596-8

Query Match      100.0%; Score 2456; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.3e-254;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAARGSPRALRLLLLVAGRCGLAGAGGAQAGLSEPPSSIAKHEDSLKDLFDYER 60
DB 1 MAARGSPRALRLLLLVAGRCGLAGAGGAQAGLSEPPSSIAKHEDSLKDLFDYER 60
QY 61 WVRPVEHLNDKIKFGLAISQLVDVDEKNQMTTNVWLKQEWIDVKLRWNPDDYGGIKV 120
DB 61 WVRPVEHLNDKIKFGLAISQLVDVDEKNQMTTNVWLKQEWIDVKLRWNPDDYGGIKV 120
QY 121 IRVPSDSVWTPDVLFDNADGRPEGTSTKTVIRYNGTVTWTPPANYKSSCTIDVTFPPFD 180
DB 121 IRVPSDSVWTPDVLFDNADGRPEGTSTKTVIRYNGTVTWTPPANYKSSCTIDVTFPPFD 180
QY 181 LQNCMKFGSWTYDGSQVDIILEDQDQVDRKDPFDNGEWEIVSATGSKGNRTDSCCWYPYV 240
DB 181 LQNCMKFGSWTYDGSQVDIILEDQDQVDRKDPFDNGEWEIVSATGSKGNRTDSCCWYPYV 240
QY 241 TYSFVIKRLPLFYTLFLIIICIGLSFLTVLVFVLPSEGEKICLCTSVLVSLVFLLVIE 300
DB 241 TYSFVIKRLPLFYTLFLIIICIGLSFLTVLVFVLPSEGEKICLCTSVLVSLVFLLVIE 300
QY 301 EIIPSSSKVPLIGEYLVFTMI FVTLSIMVTVFPAINTHRRSSSTHNAMAPLVKIFLHTL 360
DB 301 EIIPSSSKVPLIGEYLVFTMI FVTLSIMVTVFPAINTHRRSSSTHNAMAPLVKIFLHTL 360
QY 361 PKLLCMRSHVDYFTQKEETESGSGPKSSRNTLEAALNSIRYTRHMKENDVREVVEDW 420
DB 361 PKLLCMRSHVDYFTQKEETESGSGPKSSRNTLEAALNSIRYTRHMKENDVREVVEDW 420
QY 421 KFTAQVLDRLMFLTWFLFVSIGSLGFVPVIYKWNILIPVHIGNANK 468
DB 421 KFTAQVLDRLMFLTWFLFVSIGSLGFVPVIYKWNILIPVHIGNANK 468

RESULT 2
US-08-660-451A-8
; Sequence 8, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Dikette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,722

; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-596-8

Query Match      100.0%; Score 2456; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.3e-254;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAARGSPRALRLLLLVAGRCGLAGAGGAQAGLSEPPSSIAKHEDSLKDLFDYER 60
DB 1 MAARGSPRALRLLLLVAGRCGLAGAGGAQAGLSEPPSSIAKHEDSLKDLFDYER 60
QY 61 WVRPVEHLNDKIKFGLAISQLVDVDEKNQMTTNVWLKQEWIDVKLRWNPDDYGGIKV 120
DB 61 WVRPVEHLNDKIKFGLAISQLVDVDEKNQMTTNVWLKQEWIDVKLRWNPDDYGGIKV 120
QY 121 IRVPSDSVWTPDVLFDNADGRPEGTSTKTVIRYNGTVTWTPPANYKSSCTIDVTFPPFD 180
DB 121 IRVPSDSVWTPDVLFDNADGRPEGTSTKTVIRYNGTVTWTPPANYKSSCTIDVTFPPFD 180
QY 181 LQNCMKFGSWTYDGSQVDIILEDQDQVDRKDPFDNGEWEIVSATGSKGNRTDSCCWYPYV 240
DB 181 LQNCMKFGSWTYDGSQVDIILEDQDQVDRKDPFDNGEWEIVSATGSKGNRTDSCCWYPYV 240
QY 241 TYSFVIKRLPLFYTLFLIIICIGLSFLTVLVFVLPSEGEKICLCTSVLVSLVFLLVIE 300
DB 241 TYSFVIKRLPLFYTLFLIIICIGLSFLTVLVFVLPSEGEKICLCTSVLVSLVFLLVIE 300
QY 301 EIIPSSSKVPLIGEYLVFTMI FVTLSIMVTVFPAINTHRRSSSTHNAMAPLVKIFLHTL 360
DB 301 EIIPSSSKVPLIGEYLVFTMI FVTLSIMVTVFPAINTHRRSSSTHNAMAPLVKIFLHTL 360
QY 361 PKLLCMRSHVDYFTQKEETESGSGPKSSRNTLEAALNSIRYTRHMKENDVREVVEDW 420
DB 361 PKLLCMRSHVDYFTQKEETESGSGPKSSRNTLEAALNSIRYTRHMKENDVREVVEDW 420
QY 421 KFTAQVLDRLMFLTWFLFVSIGSLGFVPVIYKWNILIPVHIGNANK 468
DB 421 KFTAQVLDRLMFLTWFLFVSIGSLGFVPVIYKWNILIPVHIGNANK 468

RESULT 3
US-08-660-451A-16
; Sequence 16, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
```


RESULT 4
 US-08-487-596-16
 ; Sequence 16, Application US/08487596
 ; Patent No. 6440681
 ; GENERAL INFORMATION:
 ; APPLICANT: Eliot, Kathryn J.
 ; APPLICANT: Ellis, Steven B.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
 ; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NICOTINOL
 ; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,596
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION NUMBER: WO US94/02447
 ; FILING DATE: 08-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION NUMBER: US 08/149,503
 ; FILING DATE: 08-NOV-1993
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION NUMBER:

```

/ APPLICATION NUMBER: US 08/029,031
/ FILING DATE: 08-MAR-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/938,154
/ FILING DATE: 30-NOV-1992
/ PRIOR APPLICATION DATA: US 07/504,455
/ APPLICATION NUMBER: US 07/504,455
/ FILING DATE: 03-APR-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Seidman, Stephanie L.
/ REGISTRATION NUMBER: 33,779
/ REFERENCE/DOCKET NUMBER: 6362-9951
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 619-238-0999
/ TELEFAX: 619-238-0062
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 458 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-487-596-16

Query Match 64.4%; Score 1582; DB 4; Length 458;
Best Local Similarity 65.8%; Pred. No. 7.3e-161;
Matches 302; Conservative 62; Mismatches 67; Indels 28; Gaps 5;

QY 13 ALLLVVAVGRCLAGAGGAGQGLSEPSIAKHEDSLKDLFDYERWVRPVEHLNDKI 72
DB 6 MLVLIVL-----GIPSSATGFP--NSIAENEDALLRHLFGQYQKWRPVLHNSNDTI 54

73 KIKFGLAISQLVDVDEKNQLMTTNVWLKQEWIDVKLRWNPDDYGGIKVIRVPDSVWVTPD 132
DB 55 KYVFGLIKISQLVDVDEKNQLMTTNVWLKQEWIDVKLRWNPDDYGGIHSIKVPESLWLPD 114

133 IVLFDNADGRFECT-STKTIVRYNGTVTTPPPANYKSSCTIDVTFPPDLQNCMKRFGSW 191
DB 115 IVLFEVADGRFGSLMTKVIKSNGLVWVTPPASYKSSCTMDYTFPPFORONCSMKRFGSW 174

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Query Match 48.9%; Score 1201.5; DB 1; Length 529;
Best Local Similarity 50.5%; Pred. No. 6.3e-120;
Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;

QY 37 LSEPSIA-----KHEDSLKDLFQDYERWVRPVEHLNDKIKIKFGLAISQLVDVDE 88
DB 41 LSSPSPTALPOGSHSTETEDRLFHLPFGYNRWARPVNTSDVIVRFGLSIAQLDIVDE 100
QY 89 KNQMTNNWLKQEWIDVKLRNPDYGGIKVIRVPSDSVWTPDVLFDNADRGEGT-S 147
DB 101 KNQMTNNWLKQESDYKLRNPDGNIITSLRVPSEMIWIPDIVLYNNADGEPAVTHM 160
QY 148 TKTIVRYNGTVTWTTPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDQDV 207
DB 161 TKAHLFSTGTVHWVPPAIYKSSCSIDVTFPPDQNCMKFGSWTYDKAKIDLEQMEQTV 220
QY 208 DKRDFPDNGEWEIVSATGSKGNRTDSCC--WYPVYTVSFVIRKRLPLFTFLIIPCIGLS 265
DB 221 DLKDYWESGEWAI VNAATGYNKSKYDCCAEIYPDVYAFVIRRLPFTYINLIIPCCLIS 280
QY 266 FLTVLVFLPSNEGEKICLCTSVLVSFTVFLVIEEIPSSSKVPIPLIGEYLVFTMIFVT 325
DB 281 CLTVLVFPLPSDCGKICLCTSVLVSFTVFLVIEEIPSSSKVPIPLIGEYLVFTMIFVT 340
QY 326 LSIWTVFPAINIHRRSSSTHNAAPLVKIFLHTLPKLLCM----- 366
DB 341 LSIWTVFVNLVHRRSPSTH-TMPHWVRGALLGCVPRWLLMNRPPPPVELCHPLRLKLS 399
QY 367 -----RSHVD---RYFTQKEET-----ESGSPKSS----- 389
DB 400 SYHLESNVDAEEREVEEDRWACAGHAPSVGTCLSHGHLHSGASGPKAEALLQGE 459
QY 390 ---RNTLEAALNSIRYITRHKENDVREVVEDWKFIAQVLDRMFLFTFLFVSIVGSLG 446
DB 460 LLLSPHMQALEGVHYIADLRSEADSSVKEDWYVAMVIDRIFLWFIIVCFGLTIGL 519
QY 447 FVP 449
DB 520 FLP 522

RESULT 7

US-08-487-596-2

; Sequence 2, Application US/08487596

; Patent No. 6440681

; GENERAL INFORMATION:

; APPLICANT: Elliott, Kathryn J.

; APPLICANT: Ellis, Steven B.

; APPLICANT: Harpold, Michael M.

; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND

; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL

; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESS: Brown, Martin, Haller & McClain

; STREET: 1660 Union Street

; CITY: San Diego

; STATE: CA

; COUNTRY: USA

; ZIP: 92101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,596

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO US94/02447

; FILING DATE: 08-MAR-1994

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/149,503
;; FILING DATE: 08-NOV-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/028,031
;; FILING DATE: 08-MAR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/938,154
;; FILING DATE: 30-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/504,455
;; FILING DATE: 03-APR-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Seidman, Stephanie L.
;; REGISTRATION NUMBER: 33,779
;; REFERENCE/DOCKET NUMBER: 6362-9951
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 619-238-0999
;; TELEFAX: 619-238-0062
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 529 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: protein
;; US-08-487-596-2

Query Match 48.9%; Score 1201.5; DB 4; Length 529;

Best Local Similarity 50.5%; Pred. No. 6.3e-120;

Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;

QY 37 LSEPSIA-----KHEDSLKDLFQDYERWVRPVEHLNDKIKIKFGLAISQLVDVDE 88
DB 41 LSSPSPTALPOGSHSTETEDRLFHLPFGYNRWARPVNTSDVIVRFGLSIAQLDIVDE 100
QY 89 KNQMTNNWLKQEWIDVKLRNPDYGGIKVIRVPSDSVWTPDVLFDNADRGEGT-S 147
DB 101 KNQMTNNWLKQESDYKLRNPDGNIITSLRVPSEMIWIPDIVLYNNADGEPAVTHM 160
QY 148 TKTIVRYNGTVTWTTPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDQDV 207
DB 161 TKAHLFSTGTVHWVPPAIYKSSCSIDVTFPPDQNCMKFGSWTYDKAKIDLEQMEQTV 220
QY 208 DKRDFPDNGEWEIVSATGSKGNRTDSCC--WYPVYTVSFVIRKRLPLFTFLIIPCIGLS 265
DB 221 DLKDYWESGEWAI VNAATGYNKSKYDCCAEIYPDVYAFVIRRLPFTYINLIIPCCLIS 280
QY 266 FLTVLVFLPSNEGEKICLCTSVLVSFTVFLVIEEIPSSSKVPIPLIGEYLVFTMIFVT 325
DB 281 CLTVLVFPLPSDCGKICLCTSVLVSFTVFLVIEEIPSSSKVPIPLIGEYLVFTMIFVT 340
QY 326 LSIWTVFPAINIHRRSSSTHNAAPLVKIFLHTLPKLLCM----- 366
DB 341 LSIWTVFVNLVHRRSPSTH-TMPHWVRGALLGCVPRWLLMNRPPPPVELCHPLRLKLS 399
QY 367 -----RSHVD---RYFTQKEET-----ESGSPKSS----- 389
DB 400 SYHLESNVDAEEREVEEDRWACAGHAPSVGTCLSHGHLHSGASGPKAEALLQGE 459
QY 390 ---RNTLEAALNSIRYITRHKENDVREVVEDWKFIAQVLDRMFLFTFLFVSIVGSLG 446
DB 460 LLLSPHMQALEGVHYIADLRSEADSSVKEDWYVAMVIDRIFLWFIIVCFGLTIGL 519
QY 447 FVP 449
DB 520 FLP 522

RESULT 8

US-08-660-451A-2

; Sequence 2, Application US/08660451A

; Patent No. 6524789

; GENERAL INFORMATION:

APPLICANT: Elliott, Kathryn J.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,722
FILING DATE: 06/07/95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 529 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-660-451A-2

Query Match 48.9%; Score 1201.5; DB 4; Length 529;
Best Local Similarity 50.5%; Pred. No. 6.3e-120;
Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;
37 LSPSSIA-----KHEDSLKDFQDYERWVRPVEHLNDKIKFGLAISQVDDVE 88
41 LSPSPALPQGGSHTEBRLFKHLFGYNRWARPVNTSDVVIVRGLSIAQLDVE 100
89 KNQMTNVLKQWIDVKLRNPDYGGIKVIRVPSDVMTDVLFDNADRGFT-S 147
101 KNQMTNVLKQWSDYKLRNPDYGGIKVIRVPSDVMTDVLFDNADRGFT-S 160
148 TKTVIRNGVTTPPPANYKSSCTIDVTFPPFDLQNCMKFGSWTYGQSDVILEDDV 207
161 TKALFSTGTVHWVPPAIYKSSCTIDVTFPPFDLQNCMKFGSWTYGQSDVILEDDV 220
208 DKRDFDNGEWEIVSATSNGNRDSCC--WYPVVTYSFVKRLPLVTLFLIIPCI 265
221 DLKQWESGWAIVNATGTYNSKYDCAEYDPDVTAFVIRRLPFTYINLIIPCL 280
266 FLTIVFLPSNEGEKICLCTSVLSVTLVFLVIEEIPSSKVIPIGELYVFTMIF 325
281 CLTVLFLPSDCGEKICLCTSVLSVTLVFLVIEEIPSSKVIPIGELYVFTMIF 340
326 LSTMTVFAINIHRRSSSTNAPVRKFLHLPKLLC----- 366
341 LSVITVFLVNLHRRSSSTNAPVRKFLHLPKLLC----- 399

QY 367 -----RSHVD---RYFTQKEET-----ESGSGPKSS----- 389
Db 400 SYHLESNDVAERREVVVEEDRWACAGHVAPSVGLTCSHGLHSGASGPKAALLQGE 459
QY 390 ---RNTLEALNSIRYITHIMKENDVREVVEWDMKFTAOVLDRMFLWTFVLSVGL 446
Db 460 LLSPHMQALEGVHYIADHLRSEDADSSVKEDMKVAMVIDRFLWLFIVFCPLGTIGL 519
QY 447 FVP 449
Db 520 FLP 522

RESULT 9

US-08-464-258B-4
Sequence 4, Application US/08464258B
Patent No. 6013766
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,258B
FILING DATE: 06/05/95
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9989
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-464-258B-4

Query Match 48.0%; Score 1179; DB 3; Length 511;
Best Local Similarity 49.0%; Pred. No. 1.5e-117;
Matches 235; Conservative 70; Mismatches 107; Indels 68; Gaps 6;
37 LSPSSIAKHEDSLKDFQDYERWVRPVEHLNDKIKFGLAISQVDDVDEKNQMTN 96
26 LQQGSHTHAEDRLFKHLFGYNRWARPVNTSDVVIVRGLSIAQLDVEKNQMTN 85
97 VMLKQWIDVKLRNPDYGGIKVIRVPSDVMTDVLFDNADRGFT-STKTVIRYN 155
86 VMLKQWIDVKLRNPDYGGIKVIRVPSDVMTDVLFDNADRGFT-STKTVIRYN 145
156 GTVTVTPPANYKSSCTIDVTFPPFDLQNCMKFGSWTYGQSDVILEDDVDRKDFDN 215

Db 146 GTVHVPPAIYKSSCIDVTFPPFDOONCKMKFGSWTYDKAKIDLEQOMERTVDLDKYWES 205
QY 216 GEWEIVSATSGKNRTDSCC--WYPVYVYSFVIRKPLPFTYTLFLIIPICIGLSFLTVLVPY 273
Db 206 GEWAIINATGYSKYDCCABIIYDPVTVYFVIRRLPFLFTYTLNLIIPCLISCLTVLVPY 265
QY 274 LPSNEGEKICICTSVLSLTVLLEIIPSSKVIPLIGYLVFTMIFVTLISIMVTVF 333
Db 266 LPSECEGEKICISVLLSLTVLLEIIPSTSLVPLIGBYLLFTMIFVTLISIVTVF 325
QY 334 ANIHRRSSSTHNAAPLVRKIFLHTLPKLLQWRSVH----- 370
Db 326 VLVNHRSPSTH--MNVWRVALLGRVPRWLLMNRPLPPELHSGPDLKLSYHWELETN 384
QY 371 ----DRYFQKEETSGSG-----PKSSRNTL----- 393
Db 385 MDAGEREETEEEBEEDENICVAGLPDSSMGVLYGHGGLHURAMEPETKPSQASEILL 444
QY 394 ----BAALNSIRYIYTRHMKENDVREVVEDWKFIAQVLDRLMELTFLFVSIUGSLGLFVP 449
Db 445 SPOIKALEGVHYIADRLSEADSSVKEDWKYVAMVDRIEFLWLFIIIVCFGLGTGLFLP 504

RESULT 10
US-08-466-589-2
; Sequence 2, Application US/08466589
; Patent No. 5837489
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,589
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9950
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 528 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-466-589-2

Query Match 47.6%; Score 1169; DB 2; Length 528;
Best Local Similarity 49.9%; Pred. No. 1.9e-116;
Matches 241; Conservative 65; Mismatches 105; Indels 72; Gaps 9;

QY 37 LSEPSIA-----KHEDSLLDLPQDYERWVAPVEHLNDKIKIKFGLAISQLVDVDE 88
Db 41 LSSPSPALPOGSGSHTEDERLFHFRGYNRWARPEVNTSDVIVRFGLSIAQLDIVDE 100
QY 89 KNQMLTNNWLKOEWDVKNPDDYGGIKVIRVPSDSVWTPDIVLFDNADRGECT-S 147
Db 101 KNQMTTNNWLKQESDYKLRNPNADFGNITSLRVPSEMINIPDIVLY-NXKGEFAVTHM 159
QY 148 TKTVIRYNGTVTWTTPANYKSSCTIDVTFPPFDLQNCMKFGSWTYDGSQVDIILEDQDV 207
Db 160 TKAHLFSTGTWVHVPPAIYKSSCIDVTFPPFDOONCKMKFGSWTYDKAKIDLEQOMERTV 219
QY 208 DKRDFDNGEWEIVSATSGKNRTDSCC--WYPVYVYSFVIRKPLPFTYTLFLIIPICIGLS 265
Db 220 DLKDYSGEWEIIVNATGYSKYDCCABIIYDPVTVYFVIRRLPFLFTYTLNLIIPCLIS 279
QY 266 FLTVLVFVLPSSNEGEKICICTSVLSLTVLLEIIPSSKVIPLIGYLVFTMIFVTL 325
Db 280 CLTVLVFVLPSSDCEKICICTSVLSLTVLLEIIPSTSLVPLIGBYLLFTMIFVTL 339
QY 326 LSIMVTVEAINIHRSSSTHNAAPLVRKIFLHTLPKLLCM----- 366
Db 340 LSIVITVFLVNDHRSPTSTH-TMPHWVRGALLGCVPWLLMNRPPPVVELCHPLRLKLSF 398
QY 367 ----RSHVD--RYFTQKEET-----BSSGSPKSS----- 389
Db 399 SYHLESNVDAEEREVVVEEDRWACAGHAPSVGTLCSHGHLHSGAGSPKAEALLQEGE 458
QY 390 ---RNTLEAALNSIRYIYTRHMKENDVREVVEDWKFIAQVLDRLMELTFLFVSIUGSLGL 446
Db 459 LLLSPHMQALEGVHYIADRLSEADSSVKEDWKYVAMVDRIEFLWLFIIIVCFGLGTGL 518
QY 447 FVP 449
Db 519 FLP 521
RESULT 11
US-08-700-636-2
; Sequence 2, Application US/08700636
; Patent No. 5910582
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,636
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9368
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-700-636-2

Query Match 47.6%; Score 1169; DB 2; Length 528;
Best Local Similarity 49.9%; Pred. No. 1.9e-116;
Matches 241; Conservative 65; Mismatches 105; Indels 72; Gaps 9;

QY 37 LSPSSIA-----KHEDSLKDLFQDYERWRVVEHLNDKIKFKGLAISQLVDVDE 88
DB 41 LSPSPALPQGGSHTEDELFKHLFRGNRWARPVNTSDVIVRFGLSIAQLIDVDE 100
QY 89 KNQLMTTNVWLKQEWIDVLRWNPDDYGGIKVIRVPSDSVMTDPDVLFDNADRFECT-S 147
DB 101 KNQMTTNVWLKQEWSDYKLRWNPADFGNITSLRVPSEMIWIPDIVLY-NKXGEFAVTHM 159
QY 148 TKTIVIRNGVTWTPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDILEDDV 207
DB 160 TKAHLESTGTVHVWPPAIYKSSCSIDVTFPPDQNCMKFGSWTYDKAKIDLEQMEQTV 219
QY 208 DKRDFPDNGEWEIVSATSNGKNTDSC--WYPVTVYSFVIRKLPFLYTLFIIPICIGLS 265
DB 220 DLKDYWESGEWAIWVATGTVNSKKYDCCAEIYPDVTYAFVIRRLPFLYTLFIIPICLLIS 279
QY 266 FLTVLVFLPSNEGEKICLCTSVLVSITVFLVIEIIPSSKVIPLIGYLVFTMIFVT 325
DB 280 CLTVLVLFLPSCGEKICLCTSVLVSITVFLVIEIIPSSKVIPLIGYLVFTMIFVT 339
QY 447 FVP 449
DB 519 FLP 521

RESULT 12
US-08-467-574-2
Sequence 2, Application US/08467574
Patent No. 6023704
GENERAL INFORMATION:
APPLICANT: Eliot, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClaim
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,574
FILING DATE: June 5, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9949
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 528 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-467-574-2

Query Match 47.6%; Score 1169; DB 3; Length 528;
Best Local Similarity 49.9%; Pred. No. 1.9e-116;
Matches 241; Conservative 65; Mismatches 105; Indels 72; Gaps 9;

QY 37 LSPSSIA-----KHEDSLKDLFQDYERWRVVEHLNDKIKFKGLAISQLVDVDE 88
DB 41 LSPSPALPQGGSHTEDELFKHLFRGNRWARPVNTSDVIVRFGLSIAQLIDVDE 100
QY 89 KNQLMTTNVWLKQEWIDVLRWNPDDYGGIKVIRVPSDSVMTDPDVLFDNADRFECT-S 147
DB 101 KNQMTTNVWLKQEWSDYKLRWNPADFGNITSLRVPSEMIWIPDIVLY-NKXGEFAVTHM 159
QY 148 TKTIVIRNGVTWTPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDILEDDV 207
DB 160 TKAHLESTGTVHVWPPAIYKSSCSIDVTFPPDQNCMKFGSWTYDKAKIDLEQMEQTV 219
QY 208 DKRDFPDNGEWEIVSATSNGKNTDSC--WYPVTVYSFVIRKLPFLYTLFIIPICIGLS 265
DB 220 DLKDYWESGEWAIWVATGTVNSKKYDCCAEIYPDVTYAFVIRRLPFLYTLFIIPICLLIS 279
QY 266 FLTVLVFLPSNEGEKICLCTSVLVSITVFLVIEIIPSSKVIPLIGYLVFTMIFVT 325
DB 280 CLTVLVLFLPSCGEKICLCTSVLVSITVFLVIEIIPSSKVIPLIGYLVFTMIFVT 339
QY 326 LSIMVTVFAINIHRSSSTHNAAPLVKIFLHTLPKLLCM----- 366
DB 340 LSVITVFLVNDVHRSPSTH-TMPHWVRGALLGCVRWLLMNRPPPPVELCHPLRLKLS 398
QY 367 -----RSHVD---RYFTQKEET-----ESGSGPKSS----- 389
DB 399 SYHWLESNDVDAEREVVVEEDRWACAGHAPSVGTLCSHGHLSGASGPKAALLQGE 458
QY 390 ---RNTLEAALNSIRYITHIMKENDVREVVEWVKFIAQVLDRLMFLTFVSVIGSLG 446
DB 459 LLLSPHMQALEGVHYIADHLSRSEDADSSVKEDWKYVAMVIDRIFLWFLFIIVCFLTIGL 518
QY 447 FVP 449
DB 519 FLP 521

RESULT 13
US-09-217-345-2
Sequence 2, Application US/09217345
Patent No. 6303753
GENERAL INFORMATION:
APPLICANT: Elliot, Kathryn J.

Qy	37	LSEPSIA-----KHEDSLLDLFQDYERWRVPRVPHLNDKIKIKFGLAISQVVDVE	88
Db	41	LSSPSPTALPOGSGSHTEEDRLFKHLFRGYNWRARPVNTSDVWTVRSGLSIAQLIDVDE	100
Qy	89	KNQLMTTNWNLKQEWIDVKLRNPDDYGGIKIVRVPDSVWTPDVLFDNADGRPEGT-S	147
Db	101	KNQMMTTNWLKQEWSDYKLRNPFADFGNITSLRVPSEMIWIPDVLV-NKXGFEAVTHM	159
Qy	148	TKTVIRYNGTWTWPPANVKSCTIDVTFPPDLQNCWKMGSWTYDCGSOVDIILEDDV	207
Db	160	TKAHLFTGTVHWPPALYKSCSDIDVTFPPDQCNKXGSGWTYDKAKIDLEQMEQTV	219
Qy	208	DKRDPFDNGEWEIVSATSGKNRNTDSCC--WYPVYTVSFVKRLPLFYTLFIIPICIGLS	265
Db	220	DLKOYWESGEWALVNAATGTYNSKKVDCCAEYPDVYAFVIRRLPLFTINLIIPCLLIS	279
Qy	266	FTVLVFLYPLSNEGEKICLCTSVLVSFLVFLVLEBIIIPSSKVIPLIGEYLVFTMIPVT	325
Db	280	CLTVLAFYLPDCCGEKITLCISVLLSLTVFLLLITEIIPSTSLVPIPLIGEYLLFTMIPVT	339
Qy	326	LSIWTVTFAINIHRSSSTHNAMAPVRKI FHLTLPKLLCM-----	366
Db	340	LSIIVITVFLVNDHRSRPSPTH-TMPHWVRGALLIGCVPRWLLMNRPPPPVELCHPLRLKLSP	398

Qy	37	LSPSSIAKHEDSLLKDLFODYERWRVPVHNLNDKIKIKFGLAISQLVDVDEKQQLMTTN	96
Db	26	LTQQSGTHAEDRLFKHLFGYNRWARPVENTSDWIVRFGLSIAQLIDVDVEKQQMNTN	85
Qy	97	VWLKQEWIDVKLRNPDDYGGIKVIRVPSSVWTPDIVLFDNADRGREGT-STKTVIRYN	155
Db	86	VWLKQEWNDYNRWDPAEFGNVTSLSRVPSSMIWIPDIVLYNNADGEPAVTHMTKAHLFFT	145
Qy	156	GTVTWTPPPANYKSCSITIDVTFPPEDLQNCMSKFGSWTYDGSQVDIILEDQDVDRKDFPDN	215
Db	146	GTVHWVPPALYKSGSCSIDVTFPPDQNCQMKFGSWTYDRAKIDLEQWERTVLKLDKQWES	205

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2003, 18:38:22 ; Search time 73 Seconds
(without alignments)
1017.590 Million cell updates/sec

Title: US-09-703-951A-8

Perfect score: 2456

Sequence: 1 MAARGSPRAURLLLLV.....PVYKWNILIPVHIGNANK 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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- 2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
- 3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
- 4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
- 5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
- 6: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
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- 23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2456	100.0	468	18 AAW09024	Neuronal nicotinic
2	2456	100.0	468	23 ABB82433	Human neuronal NAC
3	2456	100.0	468	23 ABG70490	Human neuronal nic
4	1586	64.6	458	18 AAW09020	Neuronal nicotinic
5	1586	64.6	458	22 AAE12775	Human cholinergic
6	1582	64.4	458	23 ABB82437	Human neuronal NAC
7	1582	64.4	458	23 ABG70494	Human neuronal nic
8	1201.5	48.9	529	15 AAW44155	Human neuronal nic
9	1201.5	48.9	529	16 AAR73966	Alpha 2 subunit of

10	1201.5	48.9	529	18 AAW09021	Neuronal nicotinic
11	1201.5	48.9	529	23 ABB82430	Human neuronal NAC
12	1201.5	48.9	529	23 ABG31800	Human neuronal nic
13	1201.5	48.9	529	23 ABG61850	Prostate cancer-as
14	1157.5	47.1	627	18 AAW11824	Alpha4 subunit of
15	1157.5	47.1	627	18 AAW09023	Neuronal nicotinic
16	1151.5	46.9	627	18 AAW11825	Alpha4 subunit of
17	1135	46.2	494	18 AAW09018	Neuronal nicotinic
18	1135	46.2	494	23 ABB82434	Human neuronal NAC
19	1135	46.2	494	23 ABG70491	Human neuronal nic
20	1126.5	45.9	622	23 AAO17242	Modified acetylcho
21	1126.5	45.9	622	23 ABB88883	Insect nicotinic A
22	1119	45.6	631	23 AAO17244	Modified acetylcho
23	1119	45.6	631	23 ABB08884	Modified hen ACR s
24	1115	45.4	504	18 AAW09022	Neuronal nicotinic
25	1108.5	45.1	627	15 AAW44152	Human neuronal NAC
26	1108.5	45.1	627	23 ABB82432	Human neuronal nic
27	1108.5	45.1	627	23 ABG70489	Human neuronal nic
28	1099	44.7	631	23 AAO17243	Modified acetylcho
29	1098.5	44.7	622	23 AAO17245	Modified acetylcho
30	1098.5	44.7	622	23 ABB08885	Modified hen ACR s
31	1067	43.4	538	22 ABG27365	Novel human diagno
32	1062.5	43.3	479	18 AAW09019	Nicotinic acetylch
33	1054	42.9	504	15 AAW44156	Human neuronal nic
34	1050	42.8	504	23 ABB82431	Human neuronal NAC
35	1045.5	42.6	502	22 ABG70488	Human neuronal nic
36	1045.5	42.6	502	22 AAB51021	JTF-38 nAChR alpha
37	1028.5	41.9	498	18 AAW09027	Neuronal nicotinic
38	1028.5	41.9	498	23 ABB82438	Human neuronal NAC
39	1028.5	41.9	498	23 ABG70495	Human neuronal nic
40	1025.5	41.8	498	15 AAW44154	Human neuronal nic
41	1020	41.5	519	22 ABB62694	Drosophila melanog
42	1016	41.4	495	11 AAR07143	Neuronal nicotinic
43	1014	41.3	457	6 AAP50361	Human acetyl choli
44	1014	41.3	457	21 AAY56386	Human acetylcholin
45	1005	40.9	437	22 AAU69151	Human Acetylcholin

ALIGNMENTS

RESULT 1

AAW09024

ID AAW09024 standard; Protein; 468 AA.

AC AAW09024;

XX

DT 09-APR-1997 (first entry)

XX

DE Neuronal nicotinic acetylcholine receptor alpha-5 subunit.

XX

DE Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;

XX

KW ligand-gated receptor.

XX

OS Homo sapiens.

XX

PN WO9641876-A1.

XX

PD 27-DEC-1996.

XX

PF 07-JUN-1996; 96WO-US09775.

XX

PR 07-JUN-1995; 95US-0484722.

XX

PA (SIBI-) SIBIA NEUROSCIENCES INC.

XX

PI Elliott KJ, Harpold MM;

XX

DR WPI: 1997-065463/06.

XX

DR N-FSDB; AAT48238.

XX

PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -

PT used in screening to determine the effect of drugs on the receptor

XX PS Disclosure; Page 65-66; 108pp; English.

XX CC The alpha-5 subunit (AAW09024) of the human neuronal nicotinic acetylcholine receptor (nAChR) can be expressed in transformed host cells carrying alpha-5 subunit DNA (see also AA748238). Host cells, esp. mammalian cells or amphibian oocytes, expressing the recombinant alpha-5 subunit, opt. in combination with other CC recombinant alpha and/or beta subunits (see also AA09018-23, CC AA09025-27), can be used to examine the function of human AChR and CC to identify cpds. that modulate its activity.

XX SQ Sequence 468 AA;

Query Match 100.0%; Score 2456; DB 18; Length 468;
Best Local Similarity 100.0%; Pred. No. 7.6e-231;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAARGSGPRALRLLLVQLVAGRCGLAGAGGAGQGLSEPSSTAKHEDSLKDLFQDYER 60
Db 1 MAARGSGPRALRLLLVQLVAGRCGLAGAGGAGQGLSEPSSTAKHEDSLKDLFQDYER 60

Qy 61 WVRPVEHLNDKIKFGLAISQLVDVEKNQMLTNNVWLKQEWIDVKLRWNPDDYGGIKV 120
Db 61 WVRPVEHLNDKIKFGLAISQLVDVEKNQMLTNNVWLKQEWIDVKLRWNPDDYGGIKV 120

Qy 121 IRVPSDSVWTPDVLFPNADGRFGTSTKTVIRYNGTWTWTPPNYKSSCTIDVTRPPFD 180
Db 121 IRVPSDSVWTPDVLFPNADGRFGTSTKTVIRYNGTWTWTPPNYKSSCTIDVTRPPFD 180

Qy 181 LQNCMKFGSWTYDGSQVDIILEDQDDVDKDRDPDNGEWEIVSATSGKGNRTDSCCWYPYV 240
Db 181 LQNCMKFGSWTYDGSQVDIILEDQDDVDKDRDPDNGEWEIVSATSGKGNRTDSCCWYPYV 240

Qy 241 TYSFVVKRLPLFYTLFIIPICIGLSFLTVLVFVLPSPNEGEKICLCTSVLVSLTVFLLVIE 300
Db 241 TYSFVVKRLPLFYTLFIIPICIGLSFLTVLVFVLPSPNEGEKICLCTSVLVSLTVFLLVIE 300

Qy 301 EIIPSSSKVPIPLIGEYLVFTMIFVTLTIMVTVPAINIHRSSSTHNAMAPLVKIFLHTL 360
Db 301 EIIPSSSKVPIPLIGEYLVFTMIFVTLTIMVTVPAINIHRSSSTHNAMAPLVKIFLHTL 360

Qy 361 PKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHKENDVREVVEDW 420
Db 361 PKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHKENDVREVVEDW 420

Qy 421 KFTAQVLDRLMFLTWFLFVSVIGSLGLFVPVIYKWNILIPVHIGNANK 468
Db 421 KFTAQVLDRLMFLTWFLFVSVIGSLGLFVPVIYKWNILIPVHIGNANK 468

RESULT 2
ABB82433
ID ABB82433 standard; Protein; 468 AA.
AC ABB82433;
XX
DT 22-JAN-2003 (first entry)
XX
DE Human neuronal NACHR alpha5 subunit.
XX
KW Human; neuronal; nicotinic acetylcholine receptor; NACHR; drug screening;
KW immunochemistry; NACHR alpha5 subunit; receptor.
XX
OS Homo sapiens.
XX
FN WO20025266-A2.
XX
PD 01-AUG-2002.
XX
PF 29-OCT-2001; 2001WO-US50985.
XX
PR 01-NOV-2000; 2000US-0703951.

XX PA (MERI) MERCK & CO INC.

XX PI Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KJ;

XX DR WPI; 2002-698532/75.

XX DR N-PSDB; ABV73246.

XX CC Cell comprising nucleic acids encoding human alpha and beta subunits of neuronal nicotinic acetylcholine receptors, useful for in vitro screening of a drug substance in a test system specific for humans -

XX PS Examples; Page 120-122; 143pp; English.

XX CC The invention relates to a suitable host cell transfected with an isolated nucleic acid molecule comprising a sequence of nucleotides or ribonucleotides that encodes at least one alpha or beta subunit of a human neuronal nicotinic acetylcholine receptor (NACHR). The compositions and methods of the present invention, which provide a means to prepare synthetic or recombinant receptors and receptor subunits that are substantially free of contamination from many other receptor proteins, are useful for observing the effect of a drug substance on a particular subtype to perform in vitro screening of the drug substance in a test system that is specific for humans. The antibodies can be used in immunochemistry and for diagnostic and therapeutic applications. The present sequence represents a human neuronal NACHR alpha5 subunit.

XX SQ Sequence 468 AA;

Query Match 100.0%; Score 2456; DB 23; Length 468;
Best Local Similarity 100.0%; Pred. No. 7.6e-231;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAARGSGPRALRLLLVQLVAGRCGLAGAGGAGQGLSEPSSTAKHEDSLKDLFQDYER 60
Db 1 MAARGSGPRALRLLLVQLVAGRCGLAGAGGAGQGLSEPSSTAKHEDSLKDLFQDYER 60

Qy 61 WVRPVEHLNDKIKFGLAISQLVDVEKNQMLTNNVWLKQEWIDVKLRWNPDDYGGIKV 120
Db 61 WVRPVEHLNDKIKFGLAISQLVDVEKNQMLTNNVWLKQEWIDVKLRWNPDDYGGIKV 120

Qy 121 IRVPSDSVWTPDVLFPNADGRFGTSTKTVIRYNGTWTWTPPNYKSSCTIDVTRPPFD 180
Db 121 IRVPSDSVWTPDVLFPNADGRFGTSTKTVIRYNGTWTWTPPNYKSSCTIDVTRPPFD 180

Qy 181 LQNCMKFGSWTYDGSQVDIILEDQDDVDKDRDPDNGEWEIVSATSGKGNRTDSCCWYPYV 240
Db 181 LQNCMKFGSWTYDGSQVDIILEDQDDVDKDRDPDNGEWEIVSATSGKGNRTDSCCWYPYV 240

Qy 241 TYSFVVKRLPLFYTLFIIPICIGLSFLTVLVFVLPSPNEGEKICLCTSVLVSLTVFLLVIE 300
Db 241 TYSFVVKRLPLFYTLFIIPICIGLSFLTVLVFVLPSPNEGEKICLCTSVLVSLTVFLLVIE 300

Qy 301 EIIPSSSKVPIPLIGEYLVFTMIFVTLTIMVTVPAINIHRSSSTHNAMAPLVKIFLHTL 360
Db 301 EIIPSSSKVPIPLIGEYLVFTMIFVTLTIMVTVPAINIHRSSSTHNAMAPLVKIFLHTL 360

Qy 361 PKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHKENDVREVVEDW 420
Db 361 PKLLCMRSHVDRYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHKENDVREVVEDW 420

Qy 421 KFTAQVLDRLMFLTWFLFVSVIGSLGLFVPVIYKWNILIPVHIGNANK 468
Db 421 KFTAQVLDRLMFLTWFLFVSVIGSLGLFVPVIYKWNILIPVHIGNANK 468

RESULT 3
ABG70490
ID ABG70490 standard; Protein; 468 AA.
XX
AC ABG70490;
XX
DT 06-DEC-2002 (first entry)

XX Human neuronal nicotinic acetylcholine receptor alpha 5 subunit.
DE Human; neuronal nicotinic acetylcholine receptor; nAChR; receptor;
KW ion flux; alpha 5 subunit.
XX Homo sapiens.
XX US6440681-B1.
XX 27-AUG-2002.
XX 07-JUN-1995; 95US-0487596.
XX 03-APR-1990; 90US-0504455.
XX 30-NOV-1992; 92US-0938154.
XX 08-MAR-1993; 93US-0028031.
XX 08-NOV-1993; 93US-0149503.
XX (MERI) MERCK & CO INC.
XX PA
XX Elliott KJ, Ellis SB, Harpold WM;
XX WPI: 2002-711528/77.
XX N-PSDB; ABS54873.
XX Identifying antagonists or agonists of human neuronal nicotinic
acetylcholine receptors, by contacting recombinant cells with test
compound, and measuring ion flux of cells or binding of compound to
nAChR -
XX Claim 118; Column 49-52; 56pp; English.
XX The invention relates to a method for identifying compounds that are
antagonists or agonists of human neuronal nicotinic acetylcholine
receptors (nAChRs), by contacting recombinant cells with a test
compound and measuring ion flux, the electrophysiological response of the
cells or binding of the test compound to the nAChR. The recombinant
cells are produced by transfection with a nucleic acid encoding at least
one human nAChR (alpha or beta) subunit, such that the cells express an
nAChR comprising one human subunit encoded by the transfected nucleic
acid. This sequence represents the alpha 5 subunit of the human nAChR
polypeptide.
XX Sequence 468 AA;
Query Match 100.0%; Score 2456; DB 23; Length 468;
Best Local Similarity 100.0%; Pred. No. 7.6e-231;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAARGSGPRALRLLLLVOLVAGRCGLAGAGGAGQGLSEPSIAKHEDSLKDLFDYER 60
DB 1 MAARGSGPRALRLLLLVOLVAGRCGLAGAGGAGQGLSEPSIAKHEDSLKDLFDYER 60
QY 61 WVRPVEHLNDKIKIKFGLAISQLVDVDEKQLMTTNVLMKQEWIDVQLRWNPDDYGGIKV 120
DB 61 WVRPVEHLNDKIKIKFGLAISQLVDVDEKQLMTTNVLMKQEWIDVQLRWNPDDYGGIKV 120
QY 121 IRVPSDSVMTDPDVLFDNADGRFEGTSTKTVIRYNGTWTWPPANYKSCSTIDVTFPPFD 180
DB 121 IRVPSDSVMTDPDVLFDNADGRFEGTSTKTVIRYNGTWTWPPANYKSCSTIDVTFPPFD 180
QY 181 LQNCMSKFGSWTYDCGSOVDIILEDODVDKDPFDNGEIVSATSGKGNRTDSCCWYPV 240
DB 181 LQNCMSKFGSWTYDCGSOVDIILEDODVDKDPFDNGEIVSATSGKGNRTDSCCWYPV 240
QY 241 TVSFVIRKLPFLPYTLFIIPICIGLSFLTVLVPYLPSEGEKICICTSVLVSITVFLVIE 300
DB 241 TVSFVIRKLPFLPYTLFIIPICIGLSFLTVLVPYLPSEGEKICICTSVLVSITVFLVIE 300
QY 301 EIIPSSKVIPIIGLYLFTMI FVTLTSMVTVFAINIHRSSSTHNAPLVKIFLHTL 360
DB 301 EIIPSSKVIPIIGLYLFTMI FVTLTSMVTVFAINIHRSSSTHNAPLVKIFLHTL 360

QY 361 PKLLCMRSHVDYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHMKENDVREVVEDW 420
DB 361 PKLLCMRSHVDYFTQKEETESGSGPKSSRNTLEAALNSIRYITRHMKENDVREVVEDW 420
QY 421 KFAIQVLDRLMFLWTFLFVSIVGSLGLFVPVYIKWANILIPVHIGNANK 468
DB 421 KFAIQVLDRLMFLWTFLFVSIVGSLGLFVPVYIKWANILIPVHIGNANK 468
RESULT 4
AAW09020
ID AAW09020 standard; Protein; 458 AA.
XX AC AAW09020;
XX 09-APR-1997 (first entry)
XX Neuronal nicotinic acetylcholine receptor beta-3 subunit.
DE Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
KW ligand-gated receptor.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Peptide 1..20
FT /label= Sig_peptide
FT Domain 231..258
FT /label= TMD1
FT /note= "transmembrane domain 1"
FT Domain 265..287
FT /label= TMD2
FT /note= "transmembrane domain 2"
FT Domain 293..318
FT /label= TMD3
FT /note= "transmembrane domain 3"
FT Region 319..420
FT /label= Cytoplasmic_loop
FT Domain 421..446
FT /label= TMD4
FT /note= "transmembrane domain 4"
XX WO9641876-A1.
XX 27-DEC-1996.
XX 07-JUN-1996; 96WO-US09775.
XX 07-JUN-1995; 95US-0484722.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX Elliott KJ, Harpold WM;
XX WPI: 1997-065463/06.
XX N-PSDB; AAT48234.
XX Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
used in screening to determine the effect of drugs on the receptor
Claim 12; Page 79-81; 108pp; English.
XX The amino acid sequence (AAW09020) of the beta-3 subunit of the
human neuronal nicotinic acetylcholine receptor (nAChR) was deduced
from a DNA clone (AAT48234) isolated from a human substantia nigra
cDNA library. Recombinant beta-3 subunits can be expressed in host
cells, esp. mammalian cells or amphibian oocytes, optionally with
alpha-2, alpha-3, alpha-4, alpha-5, alpha-6 and/or alpha-7 subunits
(see also AAW09018-19, AAW09021-25). The recombinant subunits and host
cells can be used to study the function of the human nAChR and to
identify cpds. that modulate its activity.

Db 115 IVLFNADGRFEGSLMTKVIKNSGTWVTPPASYKSSCTMDVTFPPDRQNCMSKFGSW 174
Qy 192 TYDGSQVDIILEODVDKRFDFNGEWEIIVSATGSKGNRTDSCCWYFVTVSYFVVKELPL 251
Db 175 TYDGTWVDLLINENVDKRFDFNGEWEIILNAKMGKGNRRDGVYSPFITYSFVLRRLPL 234
Qy 252 FYTLFLIIPICIGLSFLVFLVFLYPLSPNEGEKICICTSVLSLTVFLLVIEEIIIPSSSKVIP 311
Db 235 FYTLFLIIPICIGLSFLVFLVFLYPLSPDEGEKLSLSTSVLSLTVFLLVIEEIIIPSSSKVIP 294
Qy 312 LIGELYVFTMIFVTLISMTVFAINIHRRSSSTHNAMAPLVKIFLHTLPKLLCMRSHVD 371
Db 295 LIGELYLFIWIFVTLISMTVFAINIHRRSSSTVHPWAPWVKGLFLQKLPKLLCMKDHDV 354
Qy 372 RYFT-QKEETES-----GSGPKSRNTLEALNSIRYITRHKENDVRE 415
Db 355 RYSPSEKESQPVVVGKVLKKQKQKQSDGEKVLVAFLEKAADSIRYISRHVKEHFISQ 414
Qy 416 VVEDWKFIQVLDKRMFLMTFLVSVIGSLGLFVPIVYKW 454
Db 415 VVQDWKEFVAQVLDRIFLWFLVLSATGSLVLIPTPALXKW 453

RESULT 8
AAW44155
ID AAW44155 standard; Protein; 529 AA.
XX AAW44155;
AC AAW44155;
DT 14-MAY-1998 (first entry)
XX Human neuronal nicotinic acetylcholine receptor alpha-2 subunit.
DE Human; neuronal nicotinic acetylcholine receptor; alpha-2 subunit;
KW Human; neuronal nicotinic acetylcholine receptor; alpha-2 subunit;
KW brain tissue; screening; NACHR; antibody.
XX Homo sapiens.OS Homo sapiens.XX

PH Key Location/Qualifiers
FT Peptide 1..55
FT /label= signal
FT Domain 264..289
FT /label= TWD1
FT /notes= "transmembrane domain"
FT Domain 297..320
FT /label= TWD2
FT /notes= "transmembrane domain"
FT Domain 326..350
FT /label= TWD3
FT /notes= "transmembrane domain"
FT Domain 444..515
FT /label= TWD4
FT /notes= "transmembrane domain"
FT Region 351..443
FT /label= cytoplasmic_loop
XX W09420617-A2.
XX
PD 15-SEP-1994.
XX
XX 08-MAR-1994; 94WO-US02447.
XX
XX 08-MAR-1993; 93US-0028031.
XX

XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX
XX Elliott KJ, Ellis SB, Harpold MW;
XX WPT; 1994-303024/37.
DR N-PSDB; AAV12199.
XX

PT Human neuronal nicotinic acetylcholine receptor subunits and DNA -
PT also transformed cells useful for screening cpds. which modulate
PS activity of the receptor
XX Disclosure; Page 68-70; 99pp; English.
XX
CC The present sequence represents a human neuronal nicotinic acetylcholine
CC receptor (NACHR) subunit. The cells expressing the alpha and/or beta
CC NACHR subunits may be used in a method of screening compounds to
CC identify any which modulate the activity of human neuronal NACHR.
CC Subunit specific antibodies may be used to monitor the distribution
CC and expression density of various subunits in normal vs diseased brain
CC tissues. Testing of single receptor subunits or specific receptor
CC subunit combinations with a variety of potential agonists or antagonists
CC provides information with respect to the function and activity of the
CC individual subunits and should lead to the identification and design of
CC compounds that are capable of very specific interaction with one or
CC more receptor subtypes. The resulting drugs should exhibit fewer
CC unwanted side effects than drugs identified e.g. screening with cells
XX that express a variety of subtypes.
SQ Sequence 529 AA;

Query Match 48.9%; Score 1201.5; DB 15; Length 529;
Best Local Similarity 50.5%; Pred. No. 3.2e-108;
Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;
Qy 37 LSEPSIA-----KHEDSLKDLFDYERVRVVEHLNDKIKFKGLAISQLDVDE 88
Db 41 LSSPSALPQGGSHTEDETRLFKHLFRGNRWARPVPNTSDVIVFGLSIAQLIDVDE 100
Qy 89 KNQLMTTNVWLKQEWIDVLRWNPDDYGGIKVIRVPSDSVMTDPIVLFNADGRFECT-S 147
Db 101 KNQMTTNVWLKQWSDYKLRWNPADFNITSLRVFSEMIWIDVILYNNADGEFAVTHM 160
Qy 148 TKTIVRYNGTVTWTTPPANYKSCCTIDVTFFPDLQNCMSKFGSWTYDGSQVDIILEQDV 207
Db 161 TKAHLFSTGTWVHWVPPAIYKSCSIDVTFFPQQNCCKMFGSWTYDKAKIDLEQMEQTV 220
Qy 208 DKEDFFDNGEWEIIVSATGSKGNRTDSCC--WYPVTVSYFVVKELPLFYLFIIPICIGLS 265
Db 221 DLKDYWESGEWAIIVNATGTYNSKKYDCCABEYDPVTYAFVIRLPLPYTLINLIIPCLLIS 280
Qy 266 FLTVLVFLYPLSPNEGEKICICTSVLSLTVFLLVIEEIIIPSSSKVIPILIGEYLVFTMIFVT 325
Db 281 CLTVLFLYPLSPDCGEKILCISVLSLTVFLLVIEEIIIPSTSLVPLIGEYLVFTMIFVT 340
Qy 326 LSIWTVTFAINIHRRSSSTHNAMAPLVKIFLHTLPKLLCM----- 366
Db 341 LSIWTVTFVNLVHRRSPSTH-TWPHWVRGALLGCVPRWLLMNRPPPPVELCHPLRLKLSLSP 399
Qy 367 -----RSHVD---RYFTQKEET-----ESGSGPKSS----- 389
Db 400 SYHLESNVDAAEREVVEEEDRWACAGHVAPSVTGLCSHGHLSHGASGAKAEALLQEGE 459
Qy 390 ---RNTLEAALNSIRYITRHKENDVREVEVDWKFIQVLDKRMFLMTFLVSVIGSLGL 446
Db 460 LLLSPHMQKALEGVHVIADHLSRSEDADSSVKEDWKYVAVVIDRIFLWFLVIIVCFGLTIGL 519
Qy 447 FVP 449
Db 520 FLP 522

RESULT 9
AAR73966
ID AAR73966 standard; Protein; 529 AA.
XX AAR73966;
AC AAR73966;
XX
DT 25-MAR-2003 (updated)
DT 30-NOV-1995 (first entry)
XX

DE Alpha 2 subunit of a human neuronal nicotinic acetylcholine receptor.
 XX Human nAChR; neuronal nicotinic acetylcholine receptor;
 KW neurotransmitter.

OS Homo sapiens.

XX WO9513299-A1.

XX PD 18-MAY-1995.

XX PF 08-NOV-1994; 94WO-US12859.

XX PR 08-NOV-1993; 93US-0149503.

XX PA (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.

XX PI Elliott KJ, Ellis SB, Harpold MM;

XX DR WPI; 1995-194036/25.

XX DR N-PSDB; AAQ90387.

XX New human neuronal nicotinic acetylcholine receptor alpha2 subunit DNA
 PT used to develop prods. for detection, diagnosis and therapy and for
 PT modulating activity

XX PS Disclosure; Page 43-46; 54pp; English.

XX DNA encoding the human nAChR alpha2 subunit was isolated from a
 CC human thalamus tissue cDNA library using corresp. rat cDNA. The
 CC insert of one clone obtd. was ligated with the insert of another
 CC clone to generate a full-length alpha 2 subunit cDNA. The DNA can be
 CC used to identify function nAChRs. Cells contg. the DNA can be used
 CC for screening to identify cpds. which modulate the activity of human
 CC nAChRs. The human nAChR alpha 2 subunit can be used to product
 CC antibodies which can be used in immunostochemistry, diagnosis and
 CC therapy. The nucleic acids can be used for analysing disease states
 CC and creating animal models.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 529 AA;

Query Match 48.9%; Score 1201.5; DB 16; Length 529;
 Best Local Similarity 50.5%; Pred. No. 3.2e-108;
 Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;

QY 37 LSEPSIA-----KHEDSLKDLFDQYERWVRPVEHLNDKIKIKFGLAISQLVDYDE 88
 DB 41 LSSPSPALPOGGSHSTETEDRLFHFRGYNRWARPVPNTSDVIVRFGLSIAQLIDYDE 100
 QY 89 KNQMTTNVWLKQWIDVKLRWNPDDYGGIKVIRVPSDSVWTPDIVLFDNADGRPEGT-S 147
 DB 101 KNQMTTNVWLKQWSDYKLRWNPADFGNITSLRVPSEMIWIPDIVLYNNADGEFAVTHM 160
 QY 148 TKTIVRYNGVTWTPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDQDV 207
 DB 161 TKAHLFSTGTVHVWPPAIYKSSCIDVTFPPDLQNCMKFGSWTYDRAKIDLEQMEQTV 220
 QY 208 DKRDFPDNGEWEIVSATSGKGNRTDSC--WYPVTVYSFVKIKRFLPFLIIPICIGLS 265
 DB 221 DLKDYWESGEWAIWVATGYNKSDYKDCCAEYDPDVTYAFVIRRLPFLFTINLIIPCLLIS 280
 QY 266 FLTVLVFLYLPNGEGKICLCTSVLSVLTAVFLLVIEEIIIPSSSKVPLIGEVLFVFTMIFVT 325
 DB 281 CLTVLVLFPDSCGKIKLCTSVLSVLTAVFLLVIEEIIIPSTSLVPLIGEVLLFTMIFVT 340
 QY 326 LSIWTVFPAIHHRSSSTHNAFLVRKI FLHTLPKLLCM----- 366
 DB 341 LSIWTVFVNLVHHSPSTH-TMHHVWGALIGCVPRWLLNRPVPPVLCPLRLKLP 399
 QY 367 -----RSVD--RYFTQKET-----ESGGPKSS----- 389
 DB 400 SYHWLESNVDAEEVVVEEDRWACAGHAPVSGTGLCSHGLHSGAGSPKAEALLQGE 459

QY 390 ---RNTLEAALNSIRYITRHKENDVREVVEDWKFIQAQVLDRLMPLTFLFVSIYVGLGL 446
 DB 460 LLLSPHMOKALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDRIFLWLFIVVCPFGTIGL 519
 QY 447 FVP 449
 DB 520 FLP 522

RESULT 10

AAW09021
 ID AAW09021 standard; Protein; 529 AA.

XX AC AAW09021;

XX DT 09-APR-1997 (first entry)

XX DE Neuronal nicotinic acetylcholine receptor alpha-2 subunit.

XX KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
 KW ligand-gated receptor.

XX OS Homo sapiens.

XX PN WO9641876-A1.

XX PD 27-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09775.

XX PR 07-JUN-1995; 95US-0484722.

XX PA (SIBI-) SIBIA NEUROSCIENCES INC.

XX PI Elliott KJ, Harpold MM;

XX DR WPI; 1997-065463/06.

XX DR N-PSDB; AAT48235.

XX PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
 PT used in screening to determine the effect of drugs on the receptor
 XX Disclosure; Page 49-52; 108pp; English.

XX The alpha-2 subunit (AAW09021) of the human neuronal nicotinic
 CC acetylcholine receptor (nAChR) can be expressed in transformed
 CC host cells carrying alpha-2 subunit DNA (see also AAT48235). Host
 CC cells, esp. mammalian cells or amphibian oocytes, expressing the
 CC recombinant alpha-2 subunit, opt. in combination with other
 CC recombinant alpha and/or beta subunits (see also AAW09018-20,
 CC AAW09022-27) can be used to examine the function of human AChR and
 CC to identify cpds. that modulate its activity.

XX Sequence 529 AA;

Query Match 48.9%; Score 1201.5; DB 18; Length 529;
 Best Local Similarity 50.5%; Pred. No. 3.2e-108;
 Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;

QY 37 LSEPSIA-----KHEDSLKDLFDQYERWVRPVEHLNDKIKIKFGLAISQLVDYDE 88
 DB 41 LSSPSPALPOGGSHSTETEDRLFHFRGYNRWARPVPNTSDVIVRFGLSIAQLIDYDE 100
 QY 89 KNQMTTNVWLKQWIDVKLRWNPDDYGGIKVIRVPSDSVWTPDIVLFDNADGRPEGT-S 147
 DB 101 KNQMTTNVWLKQWSDYKLRWNPADFGNITSLRVPSEMIWIPDIVLYNNADGEFAVTHM 160
 QY 148 TKTIVRYNGVTWTPPANYKSSCTIDVTFPPDLQNCMKFGSWTYDGSQVDIILEDQDV 207
 DB 161 TKAHLFSTGTVHVWPPAIYKSSCIDVTFPPDLQNCMKFGSWTYDRAKIDLEQMEQTV 220
 QY 208 DKRDFPDNGEWEIVSATSGKGNRTDSC--WYPVTVYSFVKIKRFLPFLIIPICIGLS 265

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Db 221 DLKDYWESGEWAIWVATGTVNSKKYDCCAEIYPDVTYAFVIRRLPFLYTNLIIPCLLIS 280
QY 266 FLTVLVFLPSNEGEKICLCTSVLAVSLTVPLLVLEEIIIPSSKVIPLIGEVLFVTFMIFVT 325
Db 281 CLTVLVFLPSDCGCKITLCISVLLSVTVFLLLTETIIPSTSLVPLIGEVLFVTFMIFVT 340
QY 326 LSIWTVFAINIHRRSSSTHNAAPLVKIFLHTLPKLLC----- 366
Db 341 LSIWTVFVLNVHRSFSTH-TMFWVWVGALLGCVPRWLLMNRPPPPVELCHPLRLKLS 399
QY 367 -----RSHVD---RYFTQKEET-----ESGSGPKSS----- 389
Db 400 SYHWLESNVDAEREVVVEEDRWACAGHVAPSVGTLCSHGLHSGASGPKAEALLQEGE 459
QY 390 ---RNTLEAALNSIRYITRHKENDVREVVEDWKFIAQVLDRLMFLWTLFVSVISGL 446
Db 460 LLLSPHMQALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDRIFLWLFIIIVCFLTIGL 519
QY 447 FVP 449
Db 520 FLP 522

RESULT 11
ID ABB82430
AC ABB82430;
XX 22-JAN-2003 (first entry)
XX Human neuronal NACHR alpha2 subunit.
XX Human; neuronal; nicotinic acetylcholine receptor; NACHR; drug screening;
XX immunochemistry; NACHR alpha2 subunit; receptor.
XX Homo sapiens.
XX W0200259266-A2.
XX 01-AUG-2002.
XX 29-OCT-2001; 2001WO-US0985.
XX 01-NOV-2000; 2000US-0703951.
XX (MERI ) MERCK & CO INC.
XX Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KJ;
XX WPI; 2002-698532/75.
XX N-PSDB; ABV73243.
XX Cell comprising nucleic acids encoding human alpha and beta subunits of
XX neuronal nicotinic acetylcholine receptors, useful for in vitro
XX screening of a drug substance in a test system specific for humans -
XX Examples; Page 111-113; 143pp; English.
XX The invention relates to a suitable host cell transfected with an
XX isolated nucleic acid molecule comprising a sequence of nucleotides or
XX ribonucleotides that encodes at least one alpha or beta subunit of a
XX human neuronal nicotinic acetylcholine receptor (NACHR). The compositions
XX and methods of the present invention, which provide a means to prepare
XX synthetic or recombinant receptors and receptor subunits that are
XX substantially free of contamination from many other receptor proteins,
XX are useful for observing the effect of a drug substance on a particular
XX subtype to perform in vitro screening of the drug substance in a test
XX system that is specific for humans. The antibodies can be used in
XX immunochemistry and for diagnostic and therapeutic applications. The
XX present sequence represents a human neuronal NACHR alpha2 subunit.
XX

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SQ Sequence 529 AA;
Query Match 48.9%; Score 1201.5; DB 23; Length 529;
Best Local Similarity 50.5%; Pred. No. 3.2e-108;
Matches 244; Conservative 66; Mismatches 102; Indels 71; Gaps 8;
QY 37 LSEPSIA-----KHEDSLKDLFQDYERWVRVPEHLNDKIKIKFGLAISQLVDVDE 88
Db 41 LSSPSPALPOGSGHTEDETLFKHLFRGYNRWARPVPNTSDVIVRFGLSIAQLIDVDE 100
QY 89 KQQLMTNFWLQEWIDVKLRWNPDDYGGIKVIRVPSDSVWTPDIVLFDNADGRFSGT-S 147
Db 101 KQQMNTNFWLQEWSDYKLRWNPADFGNITSLRVFSEMIWIPDIVLYNNADGEFAVTHM 160
QY 148 TKTIVRYNGTVTWTPPANYKSSCTIDVTFPPDLQNSMKFGSWTYDGSQVDIILEDDV 207
Db 161 TKAHLESTGTWVWPPAIYKSSCIDVTFPPDQCNCKMKFGSWTYDKAKIDLEQMEQTV 220
QY 208 DKRDFPDNGEWEIVSATSGKNRDTSCC--WYPVYTVSFVIRKPLPLFYTLFLIIPICIGLS 265
Db 221 DLKDYWESGEWAIWVATGTVNSKKYDCCAEIYPDVTYAFVIRRLPFLYTNLIIPCLLIS 280
QY 266 FLTVLVFLPSNEGEKICLCTSVLAVSLTVPLLVLEEIIIPSSKVIPLIGEVLFVTFMIFVT 325
Db 281 CLTVLVFLPSDCGCKITLCISVLLSVTVFLLLTETIIPSTSLVPLIGEVLFVTFMIFVT 340
QY 326 LSIWTVFAINIHRRSSSTHNAAPLVKIFLHTLPKLLC----- 366
Db 341 LSIWTVFVLNVHRSFSTH-TMFWVWVGALLGCVPRWLLMNRPPPPVELCHPLRLKLS 399
QY 367 -----RSHVD---RYFTQKEET-----ESGSGPKSS----- 389
Db 400 SYHWLESNVDAEREVVVEEDRWACAGHVAPSVGTLCSHGLHSGASGPKAEALLQEGE 459
QY 390 ---RNTLEAALNSIRYITRHKENDVREVVEDWKFIAQVLDRLMFLWTLFVSVISGL 446
Db 460 LLLSPHMQALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDRIFLWLFIIIVCFLTIGL 519
QY 447 FVP 449
Db 520 FLP 522

RESULT 12
ABG31800
ID ABG31800 standard; Protein; 529 AA.
XX AC ABG31800;
XX 06-DEC-2002 (first entry)
XX Human neuronal nicotinic acetylcholine receptor alpha 2 subunit.
XX Human; neuronal nicotinic acetylcholine receptor; nNACHR; receptor;
XX ion flux; alpha 2 subunit.
XX Homo sapiens.
XX US6440681-B1.
XX 27-AUG-2002.
XX 07-JUN-1995; 95US-0487596.
XX 03-APR-1990; 90US-0504455.
XX 30-NOV-1992; 92US-0938154.
XX 08-MAR-1993; 93US-0028031.
XX 08-NOV-1993; 93US-0149503.
XX (MERI ) MERCK & CO INC.
XX Elliott KJ, Ellis SB, Harpold MM;
XX

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Db 221 DLKDYWESGEWAIWATGTNTSKYDCCABYPDVTVAFVIRLPLFYTNLIIPCLLIS 280
 QY 266 FLTVLVPYLPNKGKICLCTSVLSLTVELLVEEIPSSKVIPLIGYLVFTMIFVT 325
 Db 281 CLIVLVPYLPNKGKICLCTSVLSLTVELLVEEIPSSKVIPLIGYLVFTMIFVT 340
 QY 326 LSIWTVFAINIHRSSSTNNAPLVRKIFLHTLPKLLCM----- 366
 Db 341 LSVITVFLVNVHRSPSTH-TMPHWVRGALLGCVPRWLLMNRPPPPVLCHEPLRLKLS 399
 QY 367 -----RSHVD---RYFTQKEET-----ESGSGPKSS----- 389
 Db 400 SYHWLESNDVAEREVEVEBEDRWACAGHAPSVGTLCSHGHLHSGAGPKAALLQEGE 459
 QY 390 ---RNTLEAALNSIRYITRIMKENDREVVEVDWKPIAQLVDRMFLWTFVSVIGSLG 446
 Db 460 LLLSPHMQKALEGVHYIADHLRSEDADSSVKEDKYYAVWIDRIFLWFIIVCFGLTIGL 519
 QY 447 FVP 449
 Db 520 FLP 522

RESULT 14
 AAW11824
 ID AAW11824 standard; Protein; 627 AA.
 XX
 AC AAW11824;
 XX
 DT 25-MAR-2003 (updated)
 DT 05-OCT-1997 (first entry)
 XX
 XX Alpha4 subunit of normal nAChR.
 XX
 XX nAChR; mutation; autosomal dominant nocturnal frontal lobe epilepsy;
 KW ADNFLE; neuronal acetylcholine receptor.
 KW
 XX Homo sapiens.
 OS
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 280
 FT /note= "Ser 248 Phe is the ADNFLE-
 FT inducing mutation (see AAW11825)"
 FT
 PN AU956247-A.
 XX
 XX 09-JAN-1997.
 XX
 XX 28-JUN-1996; 96AU-0056247.
 XX
 XX 28-JUN-1995; 95AU-0003840.
 XX
 XX (UYBO-) UNIV BONN.
 PA (UYME-) UNIV MELBOURNE.
 PA (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
 XX
 PI Steinlein OK, Mullety JC, Propping PJ, Wallace RH, Phillips HA;
 PI Sutherland GR, Scheffer IE, Berkovic SF;
 XX
 XX WPI; 1997-100506/10.
 DR N-PSDB; AAT59527.
 XX
 XX CHRNA4 gene encodes neuronal nicotinic acetylcholine receptor
 PT fragment - used in diagnosis of autosomal dominant nocturnal frontal
 PT lobe epilepsy
 XX
 XX Disclosure; Fig 13; 20pp; English.
 PS
 XX The DNA sequence of the normal nAChR is given in AAT59527,
 CC the DNA sequence of the ADNFLE-inducing mutant is given in AAT59528.
 CC Mutations at codon 248, which have the effect of replacing
 CC serine by another amino acid (e.g. phenylalanine) in the sixth
 CC amino acid of the transmembrane domain 2 (M2) of the alpha4

CC subunit of nAChR have been found to be associated with ADNFLE.
 CC The primers given in AAT59529 and AAT59530 were used in the
 CC amplification of part of exon 5.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 627 AA;
 Query Match 47.1%; Score 1157.5; DB 18; Length 627;
 Best Local Similarity 39.5%; Pred. No. 8.3e-104;
 Matches 247; Conservative 77; Mismatches 110; Indels 191; Gaps 8;
 QY 7 GPALRLLLVQLVAGRCGLAGAGQAQGLSEPPSSIAKHEDSLLLKDLFQDYRWVRPVE 66
 Db 5 GPCAPRLLPFLLLGLT-----GLLRASSHVETRAHAEERLLKCLFSGYKNSRPVA 56
 QY 67 HLNDKIKIKFGALISQLDVDEKNQIMTNNVLMKQEMIDVCLRWNPDDVGGIKVIRVPSD 136
 Db 57 NISDVVLVRFGLSIAQLIDVDEKNQMTNNVWVQEWHDYKLRWDPADENVTSIIPSE 116
 QY 127 SVWTPDIVLFDNADGRFEGTS-TKTIVRYNGTVTTPPPANYKSSCTIDVTFPPFDLQNC 185
 Db 117 LIWRPDIVLNNADGDFAVTLTKAHLFHDGRVQMTTPPAIYKSSCSIDVTFPPFDQNC 176
 QY 186 MKFGSWTYDGSQVDIILEDQDVDRKDFPONGEWEIVSATSGKGNRTDSC--WYPVTYS 243
 Db 177 MKFGSWTYDKAKIDLNNMHSRVDQLDFWESGEWVIIDAVGTNTRKYECCEAEPDITVA 236
 QY 244 FVTKRLPFLVTLIIPCIIGLSFLTVLVFLPSNEGEKICLCTSVLSVSLTVFLVTEII 303
 Db 237 FVIRRLPFLTYINLIIPCLLISCLTVLVFLPSECEKICLCTSVLSVSLTVFLVTEII 296
 QY 304 PSSKVIPLIGEYLVFTMI FVTLISIMVTVFAINIHRSSSTNNAPLVRKIFLHTLPKL 363
 Db 297 PSTSLVPLIGEYLVFTMI FVTLISIVITVFLNVHRSRPTH-TMPTWVRVFLDIVPRL 355
 QY 364 LQWR-----SHVDVRYTQKE----- 378
 Db 356 LLMKRPSVVKDCNCRLLIESMHWKMASAPRFWEPEGEPPATSGTQSLHPPSPFCVPLDVP 415
 QY 379 -----ETESGS----- 384
 Db 416 ABPGPSCKSPDQLPPQPLEAKASPHSPGRCRPHGTQAPGLAKARSLSVQHMSSPG 475
 QY 385 -----GPKSSRNT----- 392
 Db 476 EAVEGGVRCRSRISQYCVPRDDAAPEADGQAAGALASRNTSHAELPPDPQSPCKCTCK 535
 QY 393 -----LEAALNSIRYITRIMKENDREVVEVDWKPIA 424
 Db 536 EPSSVSPSATVKTSTKAPPPLPLSPALTRAVEGVQYIADHLKABDTDFSVKEDWKYVA 595
 QY 425 QVLDRMFLATFLVSVIGSLGLFVP 449
 Db 596 MVIDRIFLWFIIVCLGTGVGLFP 620

RESULT 15
 AAW09023
 ID AAW09023 standard; Protein; 627 AA.
 XX
 AC AAW09023;
 XX
 DT 09-APR-1997 (first entry)
 XX
 DE Neuronal nicotinic acetylcholine receptor alpha-4 subunit.
 KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
 KW ligand-gated receptor.
 XX
 OS Homo sapiens.
 XX
 XX WO9641876-A1.
 FN
 XX

PD 27-DEC-1996.
XX 07-JUN-1996; 96WO-US09775.
XX 07-JUN-1995; 95US-0484722.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX Elliott KJ, Harpold MM;
XX WPI; 1997-065463/06.
XX N-PSDB; AAT48237.
XX Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
PT used in screening to determine the effect of drugs on the receptor
XX
XX Disclosure; Page 58-61; 108pp; English.
XX
XX The alpha-4 subunit (AAW09023) of the human neuronal nicotinic
XX acetylcholine receptor (nAChR) can be expressed in transformed
XX host cells carrying alpha-4 subunit DNA (see also AAT48237). Host
XX cells, esp. mammalian cells or amphibian oocytes, expressing the
XX recombinant alpha-4 subunit, opt. in combination with other
XX recombinant alpha and/or beta subunits (see also AAW09018-22,
XX AAW09024-27), can be used to examine the function of human AChR and
XX to identify cpds. that modulate its activity.
SQ Sequence 627 AA;

Query Match 47.1%; Score 1157.5; DB 18; Length 627;
Best Local Similarity 39.5%; Pred. No. 8.3e-104;
Matches 247; Conservative 77; Mismatches 110; Indels 191; Gaps 8;
QY 7 GPRALRLLLLVOLVAGRCGLAGAGGAGORGLSEPPSSIAKHEDSLKDLFQDYERWVRVE 66
DB 5 GPGAPRLPPLLLLT-----GLLRASHVETRAHAERLUKLFSGYNKWSRPA 56
QY 67 HLNDKIKIFGLAISQLVDVDEKNQMTTNVWLKQEWIDVKLRMNPDDYGGIKVIRVPSD 126
DB 57 NISDVVLRFGLSIAQLIDVDEKNQMTTNVWLKQEWIDVKLRMNPDDYGGIKVIRVPSD 116
QY 127 SVWTPDIVLFDNADGRPGTS-TKTIVRYNGTVTTPPANYKSSCTIDVTFPPDLQNC 185
DB 117 LIWRPDIIVLYNADGDFATHTLKAHLFDHGRVQWTPPAIYKSSCSIDVTFPPDQNC 176
QY 186 MKFGSWTYDGSQVDIILEDDQVDKEDFFDNGEWEIVSATGSKGNEDTSCC--WYPTVYS 243
DB 177 MKFGSWTYDKAKIDVNNHRSRVDDQDFWESGEWIVDAVGYNTRKYECCEAIYPDITYA 236
QY 244 FVIRKLPFLTYLFLIIPICIGLSFLTVLVFLPSNEGEKICLCTSVLSLTVFLVIEBII 303
DB 237 FVIRKLPFLTYLFLIIPICIGLSFLTVLVFLPSNEGEKICLCTSVLSLTVFLVIEBII 296
QY 304 PSSKVIPLIGBYLFTMIFVTLSTMTVTVPAINIHRSSSTHNAAPLVKIFLHTLPKL 363
DB 297 PSTSLVIPLEIGYLLFTMIFVTLSTMTVTVPAINIHRSSSTHNAAPLVKIFLHTLPKL 355
QY 364 LCMR-----SHVDYFTQKE----- 378
DB 356 LMKRPSVVKONCRRLIESMHMKASAPRFPWPEGEPPATSGTQSLHPPSPFCVPLDVP 415
QY 379 -----ETESGS----- 384
DB 416 AEPGPKSPDOLPPQPLEAKASPHSPGCPCHPGTQAPGLAKARSLVQHMSSPG 475
QY 385 -----GPKSSRNT----- 392
DB 476 EAVEGGRCSRSIQYCVPRDDAEPADQAGALASRNTSAELPPDPQSPCKCTCK 535
QY 393 -----LEALNSIRYIYTHIMKENDVREVDWKFA 424
DB 536 EFSSVSPSATVKTSTRSTKAPPHPLPLSPALTRAEGVQVIADHLKAEDTDFSVKEDWKYVA 595

QY 425 QVLDRLMFWTLFVSVIVGSLGLFVP 449
DB 596 MVIDRIFLMFIIVCLLGTGVLFLP 620
Search completed: December 23, 2003, 21:21:09
Job time : 77 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.
OM nucleic - nucleic search, using sw model
Run on: December 23, 2003, 15:35:43 ; Search time 3995 Seconds
(without alignments)
11121.047 Million cell updates/sec

Title: US-09-703-951A-7
Perfect score: 1828
Sequence: 1 CCCGGCGGAGCTGTGGCGC.....ATCTAGTATTGTCATCCTGG 1828

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_nam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				Description	
Result No.	Score	Query Match	Length DB ID		
1	718.4	39.3	2449 11	AK080900	Mus muscu
2	608.6	33.3	941 13	B0433768	AGENCOURT
3	593.8	32.5	655 12	BW8339817	K-EST0116
4	565.4	30.9	1201 13	BX332469	BX332469

5	521.4	28.5	4589	11	AK030464	AK030464 Mus muscu
6	505.4	27.6	701	13	B0623054	B0623054 UI-H-FL1-
7	505	27.6	527	13	BX107344	BX107344 BX107344
8	502.2	27.5	713	10	BF793290	BF793290 602252976
9	493.6	27.0	744	13	B0289501	B0289501 603606675
10	485.2	26.5	538	9	AV748726	AV748726 AV748726
11	480.6	26.3	1008	13	BQ932830	BQ932830 AGENCOURT
12	467.4	25.6	755	10	BF130135	BF130135 601818142
13	459.4	25.1	542	9	AV749460	AV749460 AV749460
14	442.4	24.2	858	13	BQ225664	BQ225664 AGENCOURT
15	433.6	23.7	2257	11	AK017571	AK017571 Mus muscu
16	431.2	23.6	765	14	CA411814	CA411814 UI-H-E20-
17	425.2	23.3	496	10	BG185804	BG185804 RST4757 A
18	421.6	23.1	1280	12	BM465418	BM465418 AGENCOURT
19	417.4	22.8	918	10	BG216553	BG216553 RST36245
20	413.8	22.6	655	28	AQ529651	AQ529651 RPCI-11-3
21	402.2	22.0	597	10	BG080409	BG080409 H3053C09-
22	396.6	21.7	1194	13	BX394246	BX394246 BX394246
23	356.8	19.5	604	9	AW390530	AW390530 CM0-ST018
24	355.2	19.4	495	14	H13022	H13022 Y171F01.r1
25	352.8	19.3	577	12	BJ058493	BJ058493 BJ058493
26	344.2	18.8	698	12	BM718981	BM718981 UI-E-E01-
27	341	18.7	466	14	R19467	R19467 YG21303.r1
28	340.2	18.6	872	10	BG291447	BG291447 603387329
29	336	18.4	627	10	BG291359	BG291359 603387229
30	335.6	18.4	568	12	BI343148	BI343148 371202 MA
31	325.2	17.8	1071	12	BI522799	BI522799 603175889
32	321.4	17.6	856	29	CNS04DRH	AL286118 Tetraodon
33	317.4	17.4	541	12	BM984462	BM984462 UI-CF-DU1
34	308	16.8	2940	11	AK034228	AK034228 Mus muscu
35	308	16.8	3230	11	AK083157	AK083157 Mus muscu
36	302.6	16.6	894	13	BU912419	BU912419 AGENCOURT
37	296	16.2	564	12	BM035632	BM035632 full8a12.Y
38	289.4	15.8	326	10	BG199776	BG199776 RST19070
39	288.6	15.8	659	10	BB645442	BB645442 BB645442
40	287	15.7	1864	11	AK053497	AK053497 Mus muscu
41	287	15.7	2916	11	AK051730	AK051730 Mus muscu
42	287	15.7	3126	11	AK080415	AK080415 Mus muscu
43	283.2	15.5	854	29	CNS023CO	AL179313 Tetraodon
44	283.2	15.5	4290	11	AK029177	AK029177 Mus muscu
45	282.4	15.4	786	29	CNS04J50	AL293085 Tetraodon

ALIGNMENTS

RESULT 1
AK080900
LOCUS
DEFINITION

AK080900 2449 bp mRNA linear HTC 05-DEC-2002
Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length
enriched library, clone:B430203G01 product:NICOTINIC RECEPTOR ALPHA
5 SUBUNIT (FRAGMENT) homolog [Macaca mulatta], full insert
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK080900
AK080900.1 GI:26348860
HTC; CAP trapper.
Mus musculus (house mouse)

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED 10349636

AUTHORS

2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374

TITLE

JOURNAL
MEDLINE
PUBMED
AUTHORS
TITLE
JOURNAL
MEDLINE

PUBLISHED REFERENCE AUTHORS	11042159 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, K., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Fujiwaka, S., Inoue, K., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Yoneda, Y., Ishikawa, T., Inoue, Y., Kira, A. and Hayashizaki, Y. Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861 4
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL MEDLINE PUBLISHED REFERENCE AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Giesi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Tonita, M., Quackenbush, J., Schriml, L.M., Staabli, F., Suzuki, R., Furuno, M., Aono, H., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 21085660 11217851 5
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
JOURNAL REFERENCE AUTHORS	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2449) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]
TITLE	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
COMMENT	Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/.
FEATURES source	Location/Qualifiers 1..2449 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:B430203G01" /db_xref="taxon:10090" /clone="B430203G01" /sex="male" /tissue_type="adipose" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="4 days neonate" 152..1243 /note="unnamed protein product; NICOTINIC RECEPTOR ALPHA 5 SUBUNIT (FRAGMENT) homolog [Macaca mulatta] (SPTR Q9TUC6, evidence: FASTY, 91.9%ID, 100%length, match=555) putative" /codon_start=1 /protein_id="BAC38070.1" /db_xref="GI:26348861" /translation="MAARGRRRLRLLLMVLVLLAGRWPRPAGARGDGRPEGAST KTVRYNGVTWTPQANYKSSCTIDVTFPDLQNCMKFGSWTVYDGSVDILLEDQD VRTDPFDNGEWEIMSGSKNRTDSCWYFCITYSVFKRPLPFTYLLIPLCIGL SFTLVVFPSPNEGEKISLCTSVLSVLVFLVEEIIIPSSKVRILPGLIGLVFTMI FVTLSIMVTIFAINIHSSSTHNAMWPKIFLHKPKLCLCMKSHADRYFTQREEA EXDGGPKSRNTLEALDCLIRYTRHVVKENDREVVEDWKFIAQLVDRMFLMTFLVLS IIGTLGLFVPVIYKVAIIIVPHIGNTIK" BASE COUNT 626 a 558 c 578 g 687 t ORIGIN
CDS	Query Match 39.3%; Score 718.4; DB 11; Length 2449; Best Local Similarity 79.7%; Pred. No. 1.5e-129; Matches 875; Conservative 0; Mismatches 216; Indels 7; Gaps 2; 569 GCAGATGGAGCTTTTGAAGGACCACTAGCAAAAAGTATCATCGGTACATGACATGCGCTGTC 628 254 GGAGACGGACGTTTCGAAGGGCCAGTACGAAAACAGTGTCTCAGGTACCAATGCGCACTGTC 313 629 ACCTGACATCCACCGGCAAACTACAAAAGTCTCTGTACCATAGATGTCAGCTTTTCCCA 688 314 ACTTGACGCGGACCAAACTACAAAAGTCTTGCACTATAGATGACCTTTTCCCA 373 689 TTTGACCTTCAGAACTGTTCCATGAAATTTGGTCTTTGGACTTATGATGGATCAGAGTT 748 374 TTTGATCTCCAAATTTGCTCCATGAAATTCGGCTCATCGACGTATGATGGATCCAGGTC 433 749 GATATAATCTAGAGACCAAGATGTAGACAAGAGAGATTTTTCATATGAGAGATGG 808 434 GATATAATCTAGAGACCAAGATGTAGACAAGAGAGATTTTTCATATGAGAGATGG 493 809 GAGATTGTGAGTGCACACGAGGCAAGGAAACAGAACACGACAGCTGTTGCTGATCCG 868 494 GAAATCATGAGCGCAATGGGAGCAAGGGAACCGGACGACAGCTGCTGCTGGTACCCC 553 869 TATGTCACTTACTCATTTGTAATCAAGCGCTGCGCTCTCTTTTATACCTTGTTCCTTATA 928 554 TGCATCACCTACTCTCTTGTGATCAACGGCTGCGCTCTCTTCTACACCTGTTTCTTATC 613 929 ATACCTGTATTTGGGCTCTCATTTTTAACTGTACTTGTCTTCTATCTTCTTCAATGAA 988 614 ATACCTGTATTTGGGCTCTCGTTTCTTGACTGTGGTGTCTCTCTATCTCCCTTCAACGAA 673 989 GGTGAAAAGATTGCTCTGTCACCTTCAGTACTTGTGCTTTGACTGCTCTTCTTCTGTT 1048 674 GGTGAAAAGATTGCTCTGTCACCTTCAGTACTTGTGCTTTGACTGCTCTTCTGCTGGTG 733 1049 ATTGAAGAGATCATACCATCATCTTCAAAAGTCATACCTCTTAATTTGGAGAGTATCTGGTA 1108 734 ATTGAGAAATATATACCGTCATCTTCCAAAGTCATACCTCTGATCGGGAGTACTTGGTG 793 1109 TTTACCATGATTTTGTGTGACATGTCAATATGTTAAACCGTCTTCCTGCTATCAACATTCAT 1168 794 TTCACCATGATCTTCGTGACCCCTATCCATTTATGTTGCTACTATCTTGTCCATCAACATCCAC 853

Db	176	TGCCCCGGTCCCGCGCGGCGC-GGGCGATGCGCGCGGGGTGTCAGGCCCCGCGCGC	234
Qy	186	TCGCGCTGCTCTTGGTCCAGCTGGTCGCGGGCGCTGCGGTCTAGCGGGCGCGCGG	245
Db	235	TCGCGCTGCTCTTGGTCCAGCTGGTCGCGGGCGCTGCGGTCTAGCGGGCGCGCGG	294
Qy	246	GGGCGCGCAGAGAGATTCGTAACCTTCTTATTGCAAAACATGAAGATAGTTTGC	305
Db	295	GGGCGCGCAGAGAGATTCGTAACCTTCTTATTGCAAAACATGAAGATAGTTTGC	354
Qy	306	TTAAGGATTATTTCAGACTACGAAGATGGTTCGCTCTGTTGGAAACACCTGAATGACA	365
Db	355	TTAAGGATTATTTCAGACTACGAAGATGGTTCGCTCTGTTGGAAACACCTGAATGACA	414
Qy	366	AAATAAATAAATAATTTGCAATCTCAATTTGGTGGATGTGGATGAGAAATC	425
Db	415	AAATAAATAAATAATTTGCAATCTCAATTTGGTGGATGTGGATGAGAAATC	474
Qy	426	AGTTAATGACAAACGCTGTTGTAACAGAGATGGATGATGATAAATTAAGATGA	485
Db	475	AGTTAATGACAAACGCTGTTGTAACAGAGATGGATGATGATAAATTAAGATGA	534
Qy	486	ACCTGATGACTATGTTGAATAAAGATTATACGTTCTTCCAGACTCTGCTGACAC	545
Db	535	ACCTGATGACTATGTTGAATAAAGATTATACGTTCTTCCAGACTCTGCTGACAC	594
Qy	546	CAGACATCGTTTGTGATATGACAGATGACGCTTTTGAAGGACACAGTACGAAACA	604
Db	595	CAGACATCGTTTGTGATATGACAGATGACGCTTTTGAAGGACACAGTACGAAACA	654
Qy	605	GTCATCAGTACAAATGGCACTGTCACCTGACATCCACCGGCAAACTACAAAATGCTCTGT	664
Db	655	GTCATCAGTACAAATGGCAATTCATAGCCAGGTTCTTGATCGATGTTTCTGT	714
Qy	665	ACCATAGATGTCAGTTTCCATTGACCTTCAGAACTGT	707
Db	715	GGACTTTTCTTTTCAATGTTGGATCTCTTGGGCTTTT	757
RESULT 5			
AK030464			
LOCUS	AK030464		
DEFINITION	Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330415J08 product:NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, BETA-3 CHAIN PRECURSOR homolog [Rattus norvegicus], full insert sequence.	4589 bp	linear
ACCESSION	AK030464		
VERSION	AK030464.1	GI:26326458	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Aizawa, M., Ohara, E., Watahiki, M.,		

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	
Genome Res. 10 (11), 1757-1771 (2000)	
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yananaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, C., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Buit, C., Fletcher, C., Fujita, M., Gariboldi, M., Gusticich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.	
Functional annotation of a full-length mouse cDNA collection	
Nature 409 (6821), 685-690 (2001)	
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5	
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
Nature 420, 563-573 (2002)	
6 (bases 1 to 4589)	
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kuribayashi, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
Direct Submission	
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
Please visit our web site for further details.	
URL: http://genome.gsc.riken.go.jp/	
URL: http://fantom.gsc.riken.go.jp/	
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UI-H-FLI-bgd-k-15-0-UI 3', mRNA sequence.
ACCESSION
BU623054
VERSION
BU623054.1 GI:23289269
KEYWORDS
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SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 701)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
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Clone Distribution: Clone distribution information can be obtained from Dr. M. Banto Soares, bento-soares@iowa.edu
The following repetitive elements were found in this cDNA sequence: 1-46, >AT rich#Low_complexity
Seq primer: M13 FORWARD
POLYA=Yes.

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2. Feature 2	Source 2
3. Feature 3	Source 3
4. Feature 4	Source 4
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6. Feature 6	Source 6
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122 c 102 g 238 t

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 AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
 Rabl, U., Schneider, D. and Korn, B.
 TITLE Human Unigeneset - RZPD3
 COMMENT Unpublished
 Contact: Ina Rolf
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD; IMAGP998K02266.
 RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
 Human Unigeneset - RZPD3 (RZPDLIB No.972)
 http://www.rzpd.de/CloneCards/cgi-
 bin/showLib.pl.cgi?response?libNo=972 Contact: Ina Rolf
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de

FEATURES source

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double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lfam1d BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
117 c 99 c 173 t

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BASE COUNT	138 a	117 c	99 a	173 b
	constructed by benito soares			

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Matches 527; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Db			

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VERSION BF793290.1 GI:12098344
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9965 row: g column: 19
High quality sequence stop: 707.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4345386"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_84"
/notes="Organ: adrenal gland; Vector: pCMV-SPORT6; Site:1:
NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
221 a 117 c 164 g 211 t

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FEATURES

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/clone="IMAGE:4345386"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_84"
/notes="Organ: adrenal gland; Vector: pCMV-SPORT6; Site:1:
NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
221 a 117 c 164 g 211 t

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BASE COUNT

ORIGIN

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Query Match 27.5%; Score 502.2; DB 10; Length 713;
Best Local Similarity 97.3%; Pred. No. 1.9e-87;
Matches 532; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

QY 340 TCGTCTGTGGACACCTGAAATGACAAATAAAATTTGGACTTGGCAATATCTCA 399
Db 1 TCGTCTGTGGACACCTGAAATGACAAATAAAATTTGGACTTGGCAATATCTCA 60
QY 400 ATTGGTGGATGTGGATGAGAAAATCAGTTTATGACAAACAACTCTGGTTGAAACAGGA 459
Db 61 ATTGGTGGATGTGGATGAGAAAATCAGTTTATGACAAACAACTCTGGTTGAAACAGGA 120
QY 460 ATGGATAGATGTAAAATTAAGATGGAACCTCTGATGATATGTTGGAATAAAAGTTATACG 519
Db 121 ATGGATAGATGTAAAATTAAGATGGAACCTCTGATGATATGTTGGAATAAAAGTTATACG 180
QY 520 TGTTCCTTTCAG-ACTCTGTCTGACACACCA-CACTGTTTGTGTTTATGATATGATGGA 577
Db 181 TGTTCCTTTCAGAACTCTGTCTGACACCAAGAGCATCGTTTGTGTTTATGATATGATGGA 240
QY 578 CGTTTGAAGGGACCACTAGTACGAAAACAGTCATCAGGTACAAATGGCACTGTCACTTGGACT 637
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QY 638 CCACCGGCAAACTACAAAAGTTCTCTGTACATAGATGTCACTGTTTCCCATTTGACCTT 697
Db 301 CCACCGGCAAACTACAAAAGTTCTCTGTACATAGATGTCACTGTTTCCCATTTGACCTT 360
QY 698 CAGAACTGTTCCATGAAATTTGGTTCTTGGACTTATGATGATGATGATGATGATGATGAT 757
Db 361 CAGAACTGTTCCATGAAATTTGGTTCTTGGACTTATGATGATGATGATGATGATGATGAT 420
QY 758 CTAGAGGACCAAGATGTAGACAGAGAGATTTTGTGATAATGGAGAATGGAGATTTGTG 817
Db 421 CTAGAGGACCAAGATGTAGACAGAGAGATTTTGTGATAATGGAGAATGGAGATTTGTG 480
QY 818 AGTCAACAGGGAGCAAGAAACAGAACCGACAGCTGTTGCTGTTATCGTATGTCACCT 877
Db 481 AGTCAACAGGGAGCAAGAAACAGAACCGACAGCTGTTGCTGTTATCGTATGTCACCT 540
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Db 541 AATTCAT 547

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RESULT 9

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BU289501
LOCUS 744 bp mRNA linear EST 27-NOV-2002
DEFINITION 603606675F1 CSBQCHN55 Gallus gallus cDNA clone CHEST589f19 5', mRNA
sequence.
ACCESSION BU289501
VERSION BU289501.1 GI:25738957
KEYWORDS Gallus gallus (chicken)
SOURCE Gallus gallus
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 744)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
22335534
12445392

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REFERENCE

```

AUTHORS Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

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FEATURES
source
Location/Qualifiers
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/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="Chesf589f19"
/sex="Female"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="CSQCHN55"
/note="Organ: kidney + adrenal; Vector: pBluescript II
KS(+); Site_1: EcoRI; Site_2: NotI; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
BASE COUNT      208 a 141 c 138 g 257 t
ORIGIN
Query Match      27.0%; Score 493.6; DB 13; Length 744;
Best Local Similarity 81.4%; Pred. No. 8.7e-86;
Matches 596; Conservative 0; Mismatches 134; Indels 2; Gaps 2;
QY 562 TGATATGCAGATGGACGCTTTTGAAGGACCACTAGTACGAAACAGTCATCAGTACAAATGG 621
Db 1 TGACATGCAGATGGACGCTTTTGAAGGACCGCTCTACTAAACTGTGGTAAATATGATGG 60
QY 622 CACTGTCACTGGATCCACCGGAAACTACAAAAGTTCCTGTACATAGATGTCACGTT 681
Db 61 CACCAATGCTGGACTCCACCAAGCAATATATAAAGTTCCTGTACTATTGACGTAACCTT 120
QY 682 TTTCCTATTCACCTTCAGACTGTTCCAGTAATTTGGTCTTCCTGGACTTATGATGATC 741
Db 121 CTTTCCCTTTGACCTCCAAACTGCTCATGAAATTTGGTCTTCCTGGACTTATGATGATC 180
QY 742 ACAGCTTGATATAATTTAGAGGACCAAGATAGACAAAGAGAGATTTTTTGATAATGG 801
Db 181 CCAGCTTGATATAATTTAGAGATATGATGTTGACAAAGAGACTTTTTTGATAATGG 240
QY 802 AGAATGGAGATGTGAGTGCAACAGGAGCAAGAAACAGAACCGACAGCTGTTGCTG 861
Db 241 AGAATGGGAAATAGTGACTGCAACAGGAGCAAGGAAAGAACTGATGATGCTGCTG 300
QY 862 GTATCCGTATGCTACTACTGATTTGTAATCAAGCGCTGCTCTCTTTTATACCTTGT 921
Db 301 GTATCCCTTTGTACATATTCATTTAATAATAGACGTTTACCACCTTTTATACAGCTTGT 360
QY 922 CTTTATAATACCTGTATTTGGCTCTCATTTTTTAAGTGTACTGTCTCTATCTTCCTTC 981
Db 361 TCTCATATCTCTGTATTTGACTTCTTTCTTAAGTGTCTCTCTCTCTCTCTCTCTCTCT 420
QY 982 AAATGAAGTGAAAGATTTGCTCTGCACCTTCAGTACTGTGTCTTTGACTGTCTCTCT 1041
Db 421 AAATGAAGTGAAAGATTTTCCCT-TTAACTTCAGTCTCTGTGTATCTCTGACTGTTTCT 479
QY 1042 TCTGTTTATGAGAGATCATACCATCTCTCAAAAGTCACTCTCTAAATTTGAGAGTA 1101
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Db 540 CTTGGTGTTTACTATGATTTTGTGACATTTGTCATTTGATTAACCTGCTTTGCTATCAA 599
QY 1162 CATTTCATCATGTTCTCTCTCAACATAATATGCTATGGCGCTT-TGGTCCGCAAGATAT 1220

Db 600 TATTCATCACCGTTTCTTCATCTACACAAATGCCACCTTGGGGTTCGCAAGATAT 659
QY 1221 TTTCTCACACGTTTCCCAAACTGTTTTCATGAGAGAGTCATGTAGACAGGTACTTCACTC 1280
Db 660 TTTCTCACAAACTTCCCAAGCTGCTGTCATGAGAGAGTCATGTAGATAGATCTTTGCTC 719
QY 1281 AGAAGAGAGAA 1292
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RESULT 10
LOCUS AV748726 538 bp mRNA linear EST 19-OCT-2000
DEFINITION AV748726 NPC Homo sapiens cDNA clone NPCAAC09 5', mRNA sequence.
ACCESSION AV748726
VERSION AV748726.1 GI:10906574
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (Bases 1 to 538)
AUTHORS Song,H., Peng,Y., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N.,
Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu
,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Ye,M., Zhang,Q.,
Han,Z., Chen,Z., Hu,R. and Chen,J.
Homo sapiens NPC library cDNA clones
Unpublished
Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel.: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
Email: mshliem@stn.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.
LOCATION/Qualifiers
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/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="NPC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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Query Match      26.5%; Score 485.2; DB 9; Length 538;
Best Local Similarity 96.7%; Pred. No. 3.8e-84;
Matches 525; Conservative 0; Mismatches 10; Indels 8; Gaps 3;
QY 49 CGTTTGTCTCACACTCACACTCAGTCTGCTGATTCCTCCCAAGAGTTCGCTTCCCGCGC 108
Db 1 CGTTTGTCTCACACTCACACTCAGTCTGCTGATTCCTCCCAAGAGTTCGCTTCCCGCGC 60
QY 109 GCGCGTCGAGAGCGGCTGCCCGGTCCTCCCGCGGGCGGGCGATGGCGGCGGGG 168
Db 61 GCGCGTCGAGAGCGGCTGCCCGGTCCTCCCGCGGGCGGGCGATGGCGGCGGGG 120
QY 169 GTGAGGCGCGCGCGCTCGCGCTGCTCTTGTCTCCAGTGTGTGCGGGCGGCTGCGG 228
Db 121 GTGAGGCGCGCGCGCTCGCGCTGCTCTTGTCTCCAGTGTGTGCGGGCGGCTGCGG 180
QY 229 TCTAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 288
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Db      181 TCTANCGGGCGCGCGCGCGCGCANAGAGGATTAATCTGAACCTTCTTCTATTGCAAA 240
QY      289 ACATGAAGATAGTTTGGCTTAAGGATTTATTTCAAGACTACGAAGATGGGTTCGTCTGT 348
Db      241 ACATGAAGATAGTTTGGCTTAAGGATTTATTTCAAGACTACGAAGATGGGTTCGTCTGT 300
QY      349 GGAACACCTGAATGACAAAATAAAATAAAATTTGGACTTGGCAATATCTCAATTTGGTGA 408
Db      301 GGAACACCTGAATGACAAAATAAAATAAAATTTGGACTTGGCAATATCTCAATTTGGTGA 360
QY      409 TGTGGATGAGAAAATCAGTTAATGACAAACAAAGCTCTGTTGAAACAGGAATGGATAGA 468
Db      361 TGTGGATGAGAAAATCAGTTAATGACAAACAAAGCTCTGTTGAAACAGGAATGGATAGA 420
QY      469 TGTAAAATTAAGATGGAAACCTGATGACTACTATGGTGGAAATAAAAGTTATACGTGTTCTTC 528
Db      421 TGT---ATTAAATGGAAACCTGATGACTATGGTGGAAAT---GTTATAGTG-TCTTC 472
QY      529 AGACTCTGCTGGACACCAAGACATCGTTTGTGTAATGCAAGATGGAGCTTTTGAAG 588
Db      473 AGACTCTGTTGGACACCAAGACATCGTTTGTGTAATGCAAGATGGAGCTTTTGAAG 532
QY      589 GAC 591
Db      533 GCC 535

RESULT 11
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LOCUS      BQ932830      1008 bp      mRNA      linear      EST 21-AUG-2002
DEFINITION AGENCOURT 8858137 NIH_MGC_94 Mus musculus cDNA clone IMAGE:6465019
5', mRNA sequence.
ACCESSION BQ932830
VERSION   BQ932830.1 GI:22348213
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 1008)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: The Cepko Laboratory
           cDNA Library Preparation: Life Technologies, Inc.
           DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LHAM13987 row: a column: 20
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               Average insert size 3.3 kb. Library enriched for
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               Note: this is a NIH_MGC Library."
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Query Match      26.3%; Score 480.6; DB 13; Length 1008;
Best Local Similarity 85.1%; Pred. No. 2.9e-83;

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Matches 537; Conservative 0; Mismatches 94; Indels 0; Gaps 0;
QY      456 AGGAATGGATAGATGTAAATTAAGATGAACCCCTGATGACTATGCTGGAATAAAGTTA 515
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QY      516 TAGCTGTTCTTCCAGACTCTCTGTGGACACCAAGACATCGTTTGTGTTGTAATGCAAGATG 575
Db      61 TAGCTGTTCTTCCAGACTCTCTGTGGATCCAGACATCGTTTGTGTTGTAATGCAAGATG 120
QY      576 GACGTTTTGAAGGACCACTAGCAAAACAGTATCAGGTACAGTGCACATGTCACCTCGGA 635
Db      121 GACGTTTTGAAGGAGCCAGTACGAAACAGTGTGTCAGGTACAAATGCGACTGTCTCCTTGA 180
QY      636 CTCACCGGCAAACTACAAAGTTCTGTACACATAGATGCACGTTTTTCCCATTTTGACC 695
Db      181 CGCAGCCAGCAAACTACAAAGTTCCTGCACTATAGATGTGACCTTTTCCCATTTGATC 240
QY      696 TTCAGAACTGTTTCCATGAAATTTGGTTCTTGGACTTATGATGATCAGGTGATATAA 755
Db      241 TCCAAATTTGCTCCATGAAATTCGGCTCATGACGATGATGATGATCCAGGTCCATATAA 300
QY      756 TTCTAGAGGACCAAGATGTAGACAAGAGATTTTTTTCATATGAGATGGAGATTG 815
Db      301 TCTAGAGGACCAAGATGTGCAAGAACAGACTTTTTTGCAATGAGAAATGGAATCA 360
QY      816 TGAGTGCAACAGGGAGCAAGGAAACAGAACCGACAGCTGTTGCTGCTATCCGTATGTCA 875
Db      361 TGAGCGCAATGGGAGCAAGGGGAAACCGACGAGAGCTGCTGCTGATACCCCTGATCA 420
QY      876 CTTACTCATTTGTAATCAAGCGCTCTCTCTTTTATACCTTGTGTTCCCTTATTAATACCCCT 935
Db      421 CCTACTCTCTTGGTATCAAAACGGCTCTCTTCTACACCCCTGTTCTTATCATACCCCT 480
QY      936 GTATTGGGCTCTCATTTTAACTGTAATGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 995
Db      481 GCATCGGGCTCTGTTTCTGACTGTGTTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 540
QY      996 AGATTGTTCTCTGCACTTCAAGTACTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1055
Db      541 AGATTGTTCTCTGCACTTCAAGTACTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
QY      1056 AGATCATACCATCATCTTCAAAAGTCATACC 1086
Db      601 AAATTATACCGTCATCTTCCAAAGTCATACC 631

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DEFINITION 601818142F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041923 5',
mRNA sequence.
ACCESSION BQ932830
VERSION   BQ932830.1 GI:10969175
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 755)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT   Contact: Robert Strausberg, Ph.D.
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: ATCC
           cDNA Library Preparation: CLONETECH Laboratories, Inc.
           DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
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Db      418 ANATGGAACCTGATGACTATGTTGGAAAT--NGTTATACGTGTTCTTCAGACTCTGNN 474
QY      539 TGGACACACGACATCGTTTTTTGTTGTAATAATGCGATGGACGTTTGAAGG 588
Db      475 TGGACACACGACATCGTTTTTTGTTGTAATAATGCGATGGACGCGTTTGGGG 524

RESULT 14
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DEFINITION AGENCOURT 7593049 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6070546
5' mRNA sequence.
ACCESSION BQ225664
VERSION    BQ225664.1 GI:20407064
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 858)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished
COMMENT    Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13355 row: a column: 11
High quality sequence stop: 472.
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_68"
                     /notes="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.8 kb. Library constructed by Life
                     Technologies."
BASE COUNT  281 a 149 c 158 g 270 t
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Query Match      24.2%; Score 442.4; DB 13; Length 858;
Best Local Similarity 99.8%; Pred. No. 8.1e-76;
Matches 443; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1385 AATGATGTCGCGAGGTGTTGAAGATTGGAATTCATACCCAGGTTCTTGATCGGATG 1444
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QY      1445 TTCTCTGGGACTTCTTTTCGTTTCAATGTTGGATCTCTGGGCTTTTGTCTCTGTT 1504
Db      61 TTCTCTGGGACTTCTTTTCGTTTCAATGTTGGATCTCTGGGCTTTTGTCTCTGTT 120

QY      1505 ATTTATAAATGGGCAATATATTAAATACCAAGTTTCATATTGGAATGCAATAAGTGAAGC 1564
Db      121 ATTTATAAATGGGCAATATATTAAATACCAAGTTTCATATTGGAATGCAATAAGTGAAGC 180

QY      1565 CTCCCAGGACCTGAAGTATACATTTAGTTTAAACACATATATCTGATGGCACCTATAAA 1624
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QY      1625 ATTATGAAAATGTAAGTTATGTTAAATTTAGTTCGAAGCTTTAAACAGACTAAGTTGCTA 1684
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QY      1685 ACCTCAATTTATGTTAAACAGATGATCCATTTGAACAGTTGGCTGTATGACTGAAGTAATA 1744
Db      301 ACCTCAATTTATGTTAAACAGATGATCCATTTGAACAGTTGGCTGTATGACTGAAGTAATA 360

QY      1745 ACTGATGAGATACATTTGATCTGTGTAATAATAGCAAAATATTATCTGAACTGGACTAGTG 1804
Db      361 ACTGATGAGATACATTTGATCTGTGTAATAATAGCAAAATATTATCTGAACTGGACTAGTG 420

QY      1805 AAAAAATCTAGTATTGTTATCCTGG 1828
Db      421 AAAAAATCTAGTATTGTTATCCTGG 444

RESULT 15
AK017571
LOCUS      AK017571
DEFINITION Mus musculus 8 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:5730417K16 product:NEURONAL ACETYLCHOLINE
RECEPTOR PROTEIN, BETA-3 CHAIN PRECURSOR homolog [Rattus
norvegicus], full insert sequence.
ACCESSION  AK017571
VERSION     AK017571.1 GI:12856874
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
AUTHORS     Carninci, P. and Hayashizaki, Y.
TITLE       High-efficiency full-length cDNA cloning
JOURNAL     Meth. Enzymol. 303, 19-44 (1999)
MEDLINE     99279253
PUBMED      10349636
REFERENCE   2
AUTHORS     Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE       Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE     20499374
PUBMED      11042159
REFERENCE   3
AUTHORS     Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, K.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE       RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
PUBMED      11076861
REFERENCE   4
AUTHORS     Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G.,
Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. P., Brownstein, M. J., Bull, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 23, 2003, 16:45:16 ; Search time 1739 Seconds
(without alignments)
3502.742 Million cell updates/sec

Title: US-09-703-951A-7

Perfect score: 1828
Sequence: 1 CCCGGCGGAGCTGTGGCGC.....ATCTAGTATTGTATCTCTGG 1828

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2211978 seqs, 1666101734 residues

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1828	100.0	1828	13	US-10-349-836-7
2	557.6	30.5	1925	13	Sequence 7, Appli
3	334.6	18.3	2664	13	Sequence 15, Appl
4	324.8	17.8	2068	13	US-10-349-836-1
5	315.6	17.3	1908	13	Sequence 1, Appli
6	315.6	17.3	1908	13	US-10-349-836-3
7	315.6	17.3	2015	15	US-10-175-523-52
8	314.8	17.2	1743	13	US-10-084-817-297
9	314	17.2	1584	15	US-10-349-836-9
10	308.8	16.9	1756	10	US-10-157-031-91
11	303.2	16.6	3496	13	US-09-892-985-3
12	295	16.1	296	10	US-10-349-836-5
13	295	16.1	296	14	US-09-878-178-1659
14	295	16.1	296	15	US-10-046-935-1659
15	294.4	16.1	1667	15	US-10-146-502-1659
					Sequence 27, Appl
					Sequence 7, Appli
					Sequence 15, Appl
					US-10-349-836-15
					Sequence 1, Appli
					US-10-349-836-1
					Sequence 3, Appli
					US-10-349-836-3
					Sequence 52, Appl
					Sequence 297, App
					US-10-084-817-297
					Sequence 9, Appli
					US-10-349-836-9
					Sequence 91, Appl
					US-10-157-031-91
					Sequence 3, Appli
					US-09-892-985-3
					Sequence 5, Appli
					US-10-349-836-5
					Sequence 1659, Ap
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					Sequence 1659, Ap
					US-10-146-502-1659
					Sequence 27, Appl
					US-10-157-031-27

291.4 15.9 1350 15 US-10-199-995-1
285.2 15.6 2374 10 US-09-892-985-5
280.8 15.4 1869 10 US-09-941-179A-10
260.6 14.8 1698 13 US-10-349-836-19
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260 14.2 1869 10 US-09-941-179A-2
237.4 13.0 2448 13 US-10-349-836-13
237.4 13.0 2450 10 US-09-892-985-9
237.2 13.0 1915 13 US-10-349-836-17
236.8 13.0 1915 10 US-09-892-985-11
204.4 11.2 2077 15 US-10-198-846-10042
201.8 11.0 3700 9 US-09-303-232-3
182 10.0 1876 10 US-09-892-985-7
182 10.0 1876 13 US-10-349-836-11
182 10.0 2087 13 US-10-352-684A-55
178.8 9.8 1590 11 US-09-954-936-1
178.6 9.8 2886 9 US-09-303-232-1
174.8 9.6 1665 13 US-10-203-968-3
174.8 9.6 1915 13 US-10-203-968-6
173.6 9.5 3109 9 US-09-303-232-5
173.4 9.5 630 9 US-09-820-339A-1
159.4 8.7 1350 9 US-09-795-693-12
159.4 8.7 1350 15 US-10-156-239-12
159.4 8.7 1350 15 US-10-199-485-12
159.4 8.7 1353 13 US-10-312-088-16
159.4 8.7 2150 9 US-09-795-693-10
159.4 8.7 2150 15 US-10-156-239-10
159.4 8.7 2150 15 US-10-199-485-10
141.6 7.7 1650 10 US-09-964-824A-128
141.6 7.7 1650 13 US-09-960-706-1058

ALIGNMENTS

RESULT 1

US-10-349-836-7
Sequence 7, Application US/10349836
Publication No. US20030138911A1
GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
Harbold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/349,836
FILING DATE: 23-Jan-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/660,451A
FILING DATE: June 7, 1996
APPLICATION NUMBER: 08/484,722
FILING DATE: 07-Jun-95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062

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;
;
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1828 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: 155..1561
; OTHER INFORMATION: alpha5 subunit human neuronal
;   nicotinic acetylcholine receptor
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-349-836-7

Query Match      100.0%; Score 1828; DB 13; Length 1828;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1828; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CCCGGCGGAGCTGTGGCGGAGCGGCCCGCTGCTGCGCTGCGCCCTCGTTTGTCTCA 60
Db |
Qy 61 CGACTCACATCAGTGTGCAATCCCAAGAGTTCCCGCGCGCGGCTCGAGAG 120
Db |
Qy 61 CGACTCACATCAGTGTGCAATCCCAAGAGTTCCCGCGCGCGGCTCGAGAG 120
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Qy 121 GCGGCTCCCGCGCTCCCGCGCGCGCGGCGATGCGCGCGCGGCGTCAAGGCCCG 180
Db |
Qy 121 GCGGCTCCCGCGCTCCCGCGCGCGCGGCGATGCGCGCGCGGCGTCAAGGCCCG 180
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Qy 181 GCGGCTCCCGCTGCTGCTTGGTCCAGCTGGTCCGCGGCGCTGCGGTCTAGCGGCGC 240
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Qy 181 GCGGCTCCCGCTGCTGCTTGGTCCAGCTGGTCCGCGGCGCTGCGGTCTAGCGGCGC 240
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Qy 241 GCGGCGCGCGCGCGAGAGAGATTATCTGAACCTTCTTATTCGAAACATGAAGATAG 300
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Qy 301 TTTGCTTAAGGATTTATTCAGACTACGAAAGATGGTTCGCTCTGGAACACCTGAA 360
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Qy 301 TTTGCTTAAGGATTTATTCAGACTACGAAAGATGGTTCGCTCTGGAACACCTGAA 360
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Qy 361 TGACAAATAAAAAATTTGGACTTGGCAATATCTCAATTTGGTGGATGTGGATGAGAA 420
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Qy 361 TGACAAATAAAAAATTTGGACTTGGCAATATCTCAATTTGGTGGATGTGGATGAGAA 420
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Qy 421 AAATCAGTTAATGACAAACAAACGCTCGTGGTGAACAGAGATGGATGTAATAAATTAAG 480
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Qy 421 AAATCAGTTAATGACAAACAAACGCTCGTGGTGAACAGAGATGGATGTAATAAATTAAG 480
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Qy 481 ATGGAACCTTGATGACTATGGTGAATAAAGTTATACGTTTCCCTTCAGACTCTGCTG 540
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Db |
Qy 541 GACACACAGACATCGTTTGTGTAATGACAGATGGACGTTTGAAGGACGACGACGAA 600
Db |
Qy 601 AACAGTCAATCAGGTACATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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Qy 601 AACAGTCAATCAGGTACATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
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Qy 661 CTGTACCATAGATGTCAGGTTTTTCCATTTGACCTTCAGACTGTTCCATGAATTTGG 720
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Db |
Qy 721 TTCTTGGACTTATGATGGATCACAGGTTGTATATAATCTTAGAGGACCAAGATGTAGACAA 780
Db |

11441 GGTAAACGCTTTCGCTATCAACATTCATCATCGTTCTTCCTCAACACATTAATGCCATGGC 1200
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1561 AAGCTCCCAAGGACGTAAGTATACATTTAGTTTAAATAGTCAACATATATCTGATGCACCTA 1620
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1621 TAAAAATTTAATAATGTAAGTTATGTTTAAATTTAGTCAAGCTTTTAAACAGACTAAGTT 1680
1621 TAAAAATTTAATAATGTAAGTTATGTTTAAATTTAGTCAAGCTTTTAAACAGACTAAGTT 1680
1681 GCTAAACCTCAATTTATGTTAAACAGATGATCCATTTGAACAGTGGCTGTATGACTGAAGT 1740
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1741 AATAACCTGATGAGATACATTTGATTTGTAATAATAGCAAAATATATCTGAACTGGAAT 1800
1801 AGTGAAAAATCTAGTATTTGATCTCTGG 1828
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Db 1801 AGTGAATACTAGTATTGTTATCTCTGG 1828

RESULT 2
US-10-349-836-15
; Sequence 15, Application US/10349836
; Publication No. US20030138911A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,836
; FILING DATE: 23-Jan-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 07-Jun-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1925 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 98...1474
; OTHER INFORMATION: beta3 human neuronal nicotinic
; acetylcholine receptor
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US-10-349-836-15

Query Match 30.5%; Score 557.6; DB 13; Length 1925;
Best Local Similarity 65.2%; Pred. No. 4.5e-140;
Matches 880; Conservative 0; Mismatches 419; Indels 51; Gaps 2;

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Db 227 GTCCGCCCTGTATTACATTCTTAATGACACCATAAAGATATATTTTGGATTGAAATATCC 286

Qy 398 CAATTGGTGGATGGATGAGAAAATCAGTTAATGACAAACAGCTCTGGTTGAAACAG 457
Db 287 CAGCTTGTAGATGTGGATGAAAGAAATCAGCTGATGACAAACAAATCTGTGGCTCAACAG 346
Qy 458 GAATGGATAGATGTAATAATTAAGATGGAACCTGATGACTATGGTGGGATAAAGTTATA 517
Db 347 GAATGGACAGACCAACAGTTAGCTTGGAAATCTGATGATTATGTTGGGATCCATTTCCATT 406
Qy 518 CGTGTCTCTCAGACTCTGTCTGGACACCAAGACATCGTTTGTGTTGTAATGACAGATGA 577
Db 407 AAAGTTCCATCAGAAATCTCTGTGGCTTCTGACATAGTTCTCTTTGAAAATGCTGACGGC 466
Qy 578 CGTTTGAAGGACCAAGTACGAAACAGTATC---AGGTACATGGCACTGTCTACCTGG 634
Db 467 CGCTTGAAGGCTCCCTGATGACCAAGCTCATCGTGAATCAAAACGGAATCTGTCTCTGG 526
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Db 527 ACCCTCCCGCCAGCTACAAAAGCTCTGACCAAGTGGACGTCACGTTTTTCCCGTTCGAC 586
Qy 695 CTTCAGAACTGTTCATGAAATTTGGTTCTTGGACTTATGATGGATCACAGTTTGATATA 754
Db 587 CGACAGAACTGCTCCATGAAGTTTGGATCCTGGACTTATGATGGACCATGTTGACCTC 646
Qy 755 ATTCTAGAGACCAAGATGTAGACAGAGATTTTTTTGATAATGAGAGATGGAGATT 814
Db 647 ATTTTGATCAATGAAATGTGACAGAAAAGACTTCTTCGATAACGAGAAATGGGAAATA 706
Qy 815 GTGAGTGCAACAGGGGACAAAGGAAACAGACCGACAGCTGTTGCTGATCCGTTATGTC 874
Db 707 CTGAATGCAAAAGGGGATGAAAGGGAACAGAAAGGACGGCGTGACTCTCTATCCCTTATC 766
Qy 875 ACTTACTCATTTGTAATCAAGCGCTGCTCTCTTTTATACCTTCTTCTTCTTATAATACC 934
Db 767 AGTATTCTTCTGCTCGAGAGCGCTGCTTATTTCTATACCTCTTCTCATCATCCCC 826
Qy 935 TGTATGGGCTCTCAATTTTAACTGTACTGTTCTATCTTCTTCTTCTTCTTCTTCTTCTT 994
Db 827 TGCCTGGGCTGTCTTCTCTAACAGTTCTTGTGTTCTTATTTTACCTTCGATGAGAGAA 886
Qy 995 AAGATTTGCTCTGCACTTCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1054
Db 887 AAATCTTTCATTTTCCATCGGTTCTGTTGTTTCTCTGACAGTTTCTTCTTCTTCTTCT 946
Qy 1055 GAGATCATACCATCATCTTCAAAAGTCACTCTAAATGGAGAGATCTCTGTTATTTTACC 1114
Db 947 GAATCATCCCATGTTCTTCCAAAGTCACTCTCTCATTTGAGAGATCTCTGTTTCTATC 1006
Qy 1115 ATGATTTTGTGACACTGTCAATTTATGTTAAACCGTCTTCTGCTATCAACATTCATCAT 1174
Db 1007 ATGATTTTGTGACCTGTCTCATCATTTGTTACCGTGTGTTGTTGTTGTTGTTGTTGTT 1066
Qy 1175 TCTTCTCAACACATAATGCCATGGCGCTTGGTCCGCAAGATATTTCTTTCACAGCTT 1234
Db 1067 TCTTCTTCCAGTACCAACCCCATGGCCCTTGGGTTAAGAGGCTCTTCTTCTGAGAACTT 1126
Qy 1235 CCCAACTGCTTTCATGAGAGTCACTGATAGACAGTACT----- 1274
Db 1127 CAAATTTACTTTGATGAAAGATCATGTGATCGTACTCATCCCCAGAGAGAGAG 1186
Qy 1275 -----TCACTCAGAAAGAGAACTGAGAGTGGTAGT 1306
Db 1187 AGTCAACCCAGTAGTGAAGGCAAGTCTCGAAAAAGAAACAGACAGCTTAGTAT 1246
Qy 1307 GGACCAAAATCTTCTAGAAAACATTTGGAAGCTGGCTCAATTTCTATTTCTGCTTACATTA 1366
Db 1247 GGAGAAAAGTTCTAGTTGCTTTTTTGGAAAAGCTGCTGATTCATTTAGATACATTTTCC 1306
Qy 1367 AGACACATCATGAGGAAAATGATGTCGTTGAGGTTGTTGAGATTTGGAATTCATAGCC 1426
Db 1307 AGACATGGAAGAAGAAACATTTTATCAGCAGGTAGTACAAAGCTGGAATTTGTAGCT 1366
Qy 1427 CAGGTTCTTGATCGATGTTTCTGTGGACTTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1486

Db 1367 CAAGTCTTACCGAATCTTCTGCTGCTCTTTCTGATAGTGTACAGGCTCGGTT 1426
Qy 1487 GGGCTTTTCTGCTGTTATTTTAAATGGCAATATATAATACCAGTTCATATTGGA 1546
Db 1427 CTGATTTTACCCTGCTGTTGAAGATGTGCTACATAGTTACCATAGGAATTTAAAGA 1486
Qy 1547 AATGCAATAAGTGAACCTCCCAAGGAC 1576
Db 1487 CATAAGACTAAATTACACCTTAGACCTGAC 1516

RESULT 3

US-10-349-836-1
; Sequence 1, Application US/10349836
; Publication No. US20030138911A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,836
; FILING DATE: 23-Jan-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 07-Jun-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2664 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 555...2141
; OTHER INFORMATION: alpha2 subunit of human neuronal
; nicotinic acetylcholine receptor
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-349-836-1

Query Match 18.3%; Score 334.6; DB 13; Length 2664;
Best Local Similarity 61.3%; Pred. No. 1.8e-79;
Matches 595; Conservative 0; Mismatches 364; Indels 12; Gaps 3;

Qy 292 TGAAGATAGTTTCTTAAGGATTTATTTCAAGACTACGAAAGATGGTTCGTCTGTGGA 351
Db 728 TGAGGACCGGCTCTTCAACACACCTTTCGGGGCTACAACCGCTGGCGCGCCGGTGCC 787
Qy 352 ACACCTGAATGACAAAATAAAATTTGGACTTGCATATCTCAATTTGGTGGATGT 411
Db 788 CAACACTTCAGACGCTGGTGAATGTGCGCTTTGGACTGTCCATCGCTCAGCTCATCGATGT 847
Qy 412 GGATGAGAAAAATCAGTTAATGACAAACAAACGCTCTGGTTGAAACAGAGATGGAATAGATGT 471
Db 848 GGATGAGAGAACCAATATGATGACCAACCAACGCTCTGGCTAAACACAGAGTGGAGCGACTA 907
Qy 472 AAAATTAAGATGGAACCTCGATGACTATGTTGGAATAAAAGTTTATACGTGTTCTCTTCAGA 531
Db 908 CAAACTGCGCTGGAACCCCGCTGATTTTGGCAACATACATCTCTCAGGGTCCCTCTCTGA 967
Qy 532 CTCGTCTGGACACAGACATCGTTTTTGTGTAATGACAGATGGAGGTTTGAAGGAC 591
Db 968 GATGATCTGGATCCCGACATTTGTTCTTACAAATGACAGATGGGGAGTTTGCAGTGAC 1027
Qy 592 ---CAGTACGAAAAACAGTCATCAGGTACAAATGACCTGTCCACCTGCACTCCACGGCAAA 648
Db 1028 CACATGACCAAGGCCACCTCTTCCAGGGCATGTGCACTGGTGCCCGGCCAT 1087
Qy 649 CTACAAAAGTTCTGTACCATAGATGTACAGTTTTTCCCATTTTGACCTTCAGAACTGTTTC 708
Db 1088 CTACAAAGAGCTCTCGCAGCATCGACCTTCTTCCCTTCGACCAAGCAAACTGCAA 1147
Qy 709 CATGAAATTTGGTTCTTGGACTTATGATGATCAGAGTTGATATTAATTTAGAGNCCA 768
Db 1148 GATGAAAGTTTGGCTCTCTGGACTTATGACAAAGGCCAAGATCGACCTGGAGCAGATGGAGCA 1207
Qy 769 AGATGTAGACAAGAGAGATTTTTTTCATATGAGAGATGGAGATTTGTAGTCAACAGG 828
Db 1208 GACTGTGGACCTGAAGAGACTACTGGGAGAGCGCGAGTGGGCCATCGTCAATGCCACGGG 1267
Qy 829 GAGCAAGGAAACAGAAACCGACAGCTGTTTGC-----TGGTATCCGTATGTCTACTTACTC 882
Db 1268 CACCTACACAGCAAGAAGTACGACTGCTGGCGCGAGATCTACCCCGAGCTCACTACGC 1327
Qy 883 ATTTGTAATCAAGCGCGCTGCTCTCTTTTATACCTTGTCTTATTAATACCTGTATTGG 942
Db 1328 CTTCTGTCATCCGGCGGCTGCGGCTCTTCTACACCATCAACCTCATATCCCTGCTGCT 1387
Qy 943 GCTCTCATTTTAACTGTACTTGTCTCTCTCTTCAATGAAAGTGAAGATTTG 1002
Db 1388 CATCTCTGCTCAGTGTGCTGCTCTTACCTGCGCCCTCGAGCTGCGGCGAGAGATCAC 1447
Qy 1003 TCTCTGCACTTCAGTACTTGTGTCTTGTGACTGTCTTCTTCTTCTGTTTATTAAGAGATCAT 1062
Db 1448 GCTGTGCAATTCGGTGTCTGTCTCACTCACCGCTTCTTCTGCTGCTCATCACTGAGATCAT 1507
Qy 1063 ACCATCATTTTCAAAAGTCATACCTCTAATTTGAGAGATGCTGGTATTTTACCATGATTTT 1122
Db 1508 CCGGTCCACCTCGCTGGTCACTCCGCTCATCCGCTCATCGGCGAGTACCTGCTGTTCACCATGATCTT 1567
Qy 1123 TGTGACACTGTCAATTTATGTTAACCGCTTCTGCTATCAACATTCATCATCGTTCCTCTC 1182
Db 1568 CGTCACCTGTCCATCGTCACTACCGCTTCTGCTCAATGTGTCACACCGCTCCCGCAG 1627
Qy 1183 AACACATAATGCCATGGCGCTTTGGTCCGCAAGATATTTCTTCAACAGCTTCCCAAACT 1242
Db 1628 CACCCACA---CAATGCCCACTGGGTGCGGGGGGCGCTTCTGGGCTGTGTGCGCGGTG 1684
Qy 1243 GCTTTCATGA 1253
Db 1685 GCTTCTGATGA 1695

RESULT 4
US-09-892-985-1
; Sequence 1, Application US/09892985

Patent No. US20020111463A1
 GENERAL INFORMATION:
 APPLICANT: Elliott, Kathryn J.
 Ellis, Steven B.
 Harpold, Michael M.
 TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Heller Ehrman White & McAuliffe
 STREET: 4250 Executive Square, 7th Floor
 CITY: La Jolla
 STATE: CA
 COUNTRY: USA
 ZIP: 92037
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/892,985
 FILING DATE: 27-Jun-2001
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/217,345
 FILING DATE: 21-DEC-98
 APPLICATION NUMBER: US 08/467,574
 FILING DATE: 05-JUN-95
 APPLICATION NUMBER: US 08/466,589,
 FILING DATE: 05-JUN-95
 APPLICATION NUMBER: US 08/028,031
 FILING DATE: 08-MAR-93
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 24735-9949B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-450-8400
 TELEFAX: 619-587-5360
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2068 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: both
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 166..1752
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-892-985-1

Query Match 17.8%; Score 324.8; DB 10; Length 2068;
 Best Local Similarity 59.9%; Pred. No. 7e-77;
 Matches 580; Conservative 0; Mismatches 379; Indels 9; Gaps 2;
 292 TGAAGATAGTTGGCTTAAGGATTTATTTCAAGACTACGAAAGATGGGTTGCTGCTGTGGA 351
 339 TGAGACCGGCTTTCAACACCTTTTCGGGGCTTACACCGCTGGGCGGCCCGGTCGCC 398
 352 ACACCTGAATGACAAATAAATAAATTTGGACTTGCAATATCTCAATTTGGTGGATGT 411
 399 CAACACTTCAGACGGTGGTGGCTTTGGCTGCTCCATGCTCAGCTCATCATGATG 458
 412 GGATGAGAAATAGTAAATGACAAACAACTCTGGTTGAAACAGGAATGATGATGT 471
 459 GGATGAGAAACCAAAATGATGACCAACCACTCTGGCTAAACAGGAGTGGAGGACTA 518
 472 AAAATTAAGATGGAACCCCTGATGACTATGGTGAATAAAGTTATACGTGTTCTTCA 531
 519 CAACTGCGTGGAAACCCCGCTGATTTGGCAACATCATCTCTCAGGGTCCCTTCTGA 578

532 CTCCTCTGGACACGACATCGTTTCTTTGTAATGACAGATGACGTTTGAAGGGAC 591
 579 GATGATCTGGATCCCGACATTTCTCTCAACAACAAANNNTGGGAGTTTGCAGTACCCCA 638
 592 CAGTACGAAACAGTCATCAGTACAATGGCACTGTCACTGGACTCCACCGGCAAACTA 651
 639 CATGACCAAGGCCACCTCTCTCCACGGGCACTGTGCACTGGGTGCCCCCGGCATCTTA 698
 652 CAAAAGTTCTGTACATAGATGTCACGTTTTTCCCATTTGACCTTTCAGAACTGTTCAT 711
 699 CAAGAGCTCTGCGACATCGACGTCACCTTCTTCCCTTCGACCAAGCACTGCAAGAT 758
 712 GAAATTTGGTCTTGGACTTATGATGATGACAGGTTGATATAATTTAGAGGACCAAGA 771
 759 GAAATTTGGCTCTGGACTTATGACAGGCCCAAGATCGACCTGGAGCAGATGGAGCAGAC 818
 772 TGTAGACAAGAGAGATTTTTTTGATAATGGAGAAATGGGAGATTTGAGTGCAACAGGGAG 831
 819 TGTGGACCTGAAGGACTACTGGGAGAGCGGCGAGTGGGCCCATCGTCAATGCCACGGGAC 878
 832 CAAAGGAAACAGAACCGACAGCTGTTGC-----TGGTATCCGTATGTCACTTACTCAT 885
 879 CTACAACAGCAAGAGTACGACTGCTGCGCGAGATCTACCCGACGTCACCTACGCTT 938
 886 TGTAAATCAAGCGCTGCTCTCTTTTATACCTTGTTCCTTATAATACCTGTATTTGGGCT 945
 939 CGTCATCCGGCGGCTGCGGCTCTTCTACACCATCAACCTCATCATCCCTGCTGCTCAT 998
 946 CTCATTTTAACTGCTACTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1005
 999 CTCCTGCTCACTGTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1058
 1006 CTGCACCTTCAGTACTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGT 1065
 1059 GTGCATTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1118
 1066 ATCATTTCAAAAGTCATACCTCTAAATTTGGAGAGTATCTGTTATTTACCATGATTTTGT 1125
 1119 GTCCACCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1178
 1126 GACACTGTCAATTTGTAACGCTTTCGCTTCAACATTTCAACATTTCACTGCTTCTTCTCAAC 1185
 1179 CACCTGTCCATCGTCATCACCGTCTTGTGCTCAATGTGGACCAACCGCTCCCCAGCAC 1238
 1186 ACATAATGCCATGGCGCTTTGCTCGCAAGATATTTCTTCAACGCTTCCCAAACTGCT 1245
 1239 CCACA---CCATGCCCACTGGGTGCGGGGGGGGCTTCTGCGGCTGTGCTGCGGCTGCT 1295
 1246 TTGCATGA 1253
 1296 TCTGATGA 1303

RESULT 5

US-10-349-836-3
 ; Sequence 3, Application US/10349836
 ; Publication No. US20030138911A1
 ; GENERAL INFORMATION:

APPLICANT: Elliott, Kathryn J.
 Harpold, Michael M.

TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

Query Match									
Best Local Similarity 17.3%; Score 315.6; DB 15; Length 1908;									
Matches 588; Conservative 0; Mismatches 384; Indels 12; Gaps 3;									
Qy	285	CAAAACATGAGATAGTTTGGCTTAAGGATTTATTTCAAGACTACGAAGATGGGTTCGTC	344						
Db	281	CAGAGCTGAGCACCGTCTATTGAGCGGCTGTTTGAAGATTACAAATGAGATCATCCGGC	340						
Qy	345	CTGTGGAAACACCTGAATGACAAATAAAATTTGGACTTGCATATATCTCAATGG	404						
Db	341	CTGTAGCCAACTGTCTGACCCAGTCATCATCTTCGAGGTGTCCATGCTCAGCTGG	400						
Qy	405	TGATGTGATGAGAAAATCAGTTAATGACAAACAACTCTGTGTTGAAACAGGAATGA	464						
Db	401	TGAAGGTGATGAAGTAAACCAAGATCATGGAGCAACCTGTGGCTCAAGCAAAATCTGA	460						
Qy	465	TAGATGTAAATTAAGATGGAACCTGTGACTATGTTGGATGAATAAAGTTATACGTGTC	524						
Db	461	ATGACTACAGCTGAAGTGGAAACCCCTCTGACTATGGTGGGCGAGTTTCATGCGTGCC	520						
Qy	525	CTTCAGACTCTCTGGACACAGACATCGTTTGTGTTGATTAATGACAGATGGACGTTTG	584						
Db	521	CTGCACAGAGATCTGGAAGCCAGACATTTGCTGTATAACAAATGCTGTGGGATTTCC	580						
Qy	585	AAGG---ACCAAGTACGAAAACAGTCATCAGGTACAATGGCACTGTCACCTGGACTCCAC	641						
Db	581	AGGTGGACGACAAAGCAAGCCTTACTCAAGTACACTGGGAGGTGACTTGGATACCTC	640						
Qy	642	CGGCAAACTACAAAGTCTGTACCATAGATGTCAGCTTTTCCATTTGACCTTCAGA	701						
Db	641	CGGCACTCTTTAAGAGCTCTGTAAATTCGACGTGACCTACTTCCCGTTTGAATACCAA	700						
Qy	702	ACTGTTCCATGAAATTTGGTCTTGGACTTATGATGGATCAAGTGTGATATAATTTAG	761						
Db	701	ACTGTACCATGAGTTGGTTCCTGCTCTAGATAAGCGGAATCATCTGTCCTGA	760						
Qy	762	AGGACCAAGATGAGCAAGAGAGATTTTGTGATAATGGAAATGGGAGATTTGAGTG	821						
Db	761	TGGCTCTTCCATGAACTCAAGGACTATTGGGAGCGGCGAGTGGGCCATCATCAAG	820						
Qy	822	CAACAGGAGGCAAGAAACAGACCGACAGCTGTGTCTG-----TATCGTATGTCA	875						
Db	821	CCCCAGGCTCAACACACGACATCAAGTACAACTGCTGGAGGAGATCTACCCCGACATCA	880						
Qy	876	CTTACTCATTTGTAATCAAGCGCTGCTCTCTTTTATACCTTGTCTTATAATACCT	935						
Db	881	CATCTCGCTGATACATCGGCGCTGCTGCTTCTTACCAATCAACCTCATCATCCCT	940						
Qy	936	GTTATGGCTCTCATTTTAACTGPACTTGTCTCTATCTTCTTCAAAATGAAGTGAAA	995						
Db	941	GCCTGCTCATCTCTCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1000						
Qy	996	AGATTGTCTGACATTCAGTACTTGTGCTTGTGACTGTCTTCTCTGTTTATGAG	1055						
Db	1001	AGGTGACCTGTGCAATTTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1060						
Qy	1056	AGATCATACCATCATCTTCAAAAGTCATACCTCTAAATTTGGAGAGTATCTGTTATTACA	1115						
Db	1061	AGACCATCCCTTCCACCTCGTGTGTCATCCCTGATTTGGAGAGTACCTCTGTTTACCA	1120						
Qy	1116	TGATTTTGTGACACTGTCAATTAATGTAACCGTCTTCGCTATCAACATTCATCATCGTT	1175						
Db	1121	TGATTTTGTAACTTGTCCATCTGTCATACCGCTCTCTGCTCAACGTGACATACAGAA	1180						
Qy	1176	CTTCTCAACACATATGCGATGGCGCTTTGGTCCGCAAGATATTTCTTCAACGCTTC	1235						
Db	1181	CCCCAGAC	1237						
Qy	1236	CCAAACTGCTTTGATGAGAGTC	1259						
Db	1238	CCAGGTCATGTTTATGACCGGC	1261						

RESULT 7
US-10-084-817-297
; Sequence 297, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 297
; LENGTH: 2015
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 1292280CB1
US-10-084-817-297

Query Match									
Best Local Similarity 17.3%; Score 315.6; DB 15; Length 2015;									
Matches 588; Conservative 0; Mismatches 384; Indels 12; Gaps 3;									
Qy	285	CAAAACATGAGATAGTTTGGCTTAAGGATTTATTTCAAGACTACGAAGATGGGTTCGTC	344						
Db	215	CAGAGCTGAGCACCGTCTATTTCAGCGGCTGTTTGAAGATTACAAATGAGATCATCCGGC	274						
Qy	345	CTGTGGAAACACCTGAATGACAAATAAAATTTGGACTTGCATATATCTCAATGG	404						
Db	275	CTGTAGCCAACTGTCTGACCCAGTCATCATCTTCGAGGTGTCCATGCTCAGCTGG	334						
Qy	405	TGATGTGAGTGAATAAATCAAGTTATGACAAACAACTGCTGTTGAACAGGAATGA	464						
Db	335	TGAAGGTGGATGAAGTAAACCAAGATCATGGAGCAACCTGTGCTCAAGCAAAATCTGA	394						
Qy	465	TAGATGTAAATTAAGATGGAACCCCTGATGACTATGTGGAATAAAAGTTATACGTGTC	524						
Db	395	ATGACTACAGCTCAAGTGGNACCCCTCTGACTATGTGGGCGAGAGTTTCATGCTGTC	454						
Qy	525	CTTCAGACTCTGCTGACACACAGACATCGTTTGTGTTGTAATGCAAGATGGAAGTTTG	584						
Db	455	CTGCACAGAAAGATCTGGAAGCCAGACATTTGCTGTATACAAATGCTGTGGGATTTCC	514						
Qy	585	AAGG---ACCAAGTACGAAAACAGTCATCAGGTACATGGCACTGTACCTGGACTCCAC	641						
Db	515	AGGTGGACGACAAAGCCCTTACTCAAGTACACTGGGAGGTGACTTGGATACCTC	574						
Qy	642	CGGCAAACTACAAAGTTCCTGTACCATAGATGTCAGCTTTTCCCATTTGACCTTCAGA	701						
Db	575	CGGCCATCTTTAGAGCTCTCTGTAATCGACGTGACTTCTCCGTTTGTATTACCAA	634						
Qy	702	ACTGTTCCATGAAATTTGGTCTTGTGACTTATGATGGATCACAGTTTGATATAATTTAG	761						
Db	635	ACTGTACCATGAAGTTCGGTTCCTGCTCTACGATAAGCGGAAATCGATCTGCTGCTGA	694						
Qy	762	AGGACCAAGATGTAGACAAAGAGATTTTGTGATGATGAGATGGAGATTTGAGTG	821						
Db	695	TCGGCTCTTCCATGAACCTCAAGGACTATTTGGGAGACGCGGAGTGGGCCATCATCAAAG	754						
Qy	822	CAACAGGAGCAAGGAAACAGAACCCAGACAGCTGTGCTG-----TATCCGTATGTCA	875						
Db	755	CCCCAGGCTCAACACACGACATCAAGTACAACTGCTGCGAGGAGATCTACCCCGACATCA	814						
Qy	876	CTTACTCATTTGTAATCAAGCGCTGCTCTCTTTTATACCTTGTCTTATAATACCT	935						

TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-450-8400
TELEFAX: 619-587-5360
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1756 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 39..1553
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-892-985-3

Query Match 16.9%; Score 308.8; DB 10; Length 1756;
Best Local Similarity 59.2%; Pred. No. 1.4e-72;
Matches 583; Conservative 1; Mismatches 388; Indels 12; Gaps 3;

QY 285 CAAAACATGAAGTAGTTTCCTTAAGGATTATTTCAAGACTACGAAAGATGGTTTCGTC 344
DB 130 CAGAGGCTGAGACCGCTCTATTGAGCGGCTGTTGAAGATTACAATGAGATCATCGGC 189
QY 345 CTGTGGAACACCTGAATGACAAAATAAAATTAATTTGACTTGCAATATCTCAATTGG 404
DB 190 CTGTGGCCACAGTGTGACCCAGTATCATTCATTTGAGGTGTCATGTCCTCAGCTGG 249
QY 405 TGGATGTGGATGAGAAAATCAGTTAATGACAAACAACTGCTGTTGAAACAGGAATGGA 464
DB 250 TGAAGGTGGATGAAGTAAACAGATCATGAGACCAACCTGTGGCTCAAGCAAAATCTGM 309
QY 465 TAGATGTAAATTAAGATGAAACCTGATGACTATGTTGGAATAAAGATTATAGGTTC 524
DB 310 ATGACTACAAAGTGAAGTGAACCCCTCTGACTATGTTGGGCGAGATTATCGGTGTC 369
QY 525 CTTCAGACTCTGCTGACACACGACATCGTTTGTGTTGATAATGACAGATGGAGTTTG 584
DB 370 CTGCACAGAGACTGAGAGCCAGACATTTGCTGTATACATGCTGTTGGGATTTCC 429
QY 585 AAGG---ACCAGTACGAAACAGTCAATGAGTCAATGACCTGTGACCTGGACTCCAC 641
DB 430 AGGTGGACGACAGACCAAGCCCTTACTCAAGTACACTGGGAGGTGACTTGGATACCTC 489
QY 642 CGGCAACTACAAAGTTCCTGTACATAGATGATGCTGTTTCCCATTTGACCTTCAGA 701
DB 490 CGGCCATCTTTAAGAGCTCCTGTAATAATCGACGTGACCTACTTCCCGTTTGTATACCAA 549
QY 702 ACTGTTCCATGAATTTGGTTCTTGGACTTATGATGATCAGAGTTGATATAATCTAG 761
DB 550 ACTGTACATGAAGTTCGGTTCTGCTGCTACGTAAGGAGGAAATCGACTGTCCTGA 609
QY 762 AGGACCAAGATGTAGACAGAGAGATTTTTTGATAATGAGAGATGGGAGATTGTAGTG 821
DB 610 TCGGCTCTTCCATGAACCTCAAGSACTATTGGGAGAGCGGAGTGGGCCATCATCAAG 669
QY 822 CAACAGGAGCAAGGAAACAGACCGACAGCTGTTCTGCG-----TATCCGTATGTC 875
DB 670 CCCAGGYTATAACACGACATCAAGTACAACTGCTCGAGGAGATCTACCCGACATCA 729
QY 876 CTTACTCTATTGTAATCAAGCGCTGCTCTTTTATACCTTCTCTTATATACCT 935
DB 730 CATCTCGTGATCATCGGGCGGTGCTGTTGTTCTACACCATCATCTCATCCCT 789
QY 936 GTATGGGCTCTCATTTTTTAACGTACTGTGCTCTATCTCTCTTCAAAATGAAGTGA 995
DB 790 GGCTGATCATCTCCTTCATCACTGTGTGCTCTTCTACCTGCGCTCCGACTGCGGTG 849
QY 996 AGATTGCTCTGACATTCAGTACTGTGCTGTTGACTGCTCTCTCTCTGTTATGAAG 1055
DB 850 AGGTGACCTGTGCAATTTCTGCTCCTCTCTCTGAGGCTGTTCTCTCTGATCACTG 909

1056 AGATCATACCATCATCTTCAAAAGTCATACCTCTAATTCGAGAGATATCTGGTATTTACCA 1115
DB 910 AGACCATCTTCCACCTCGTGGTTCATCCCTGATTGGAGAGTACCTCTCTGTTACCA 969
QY 1116 TGATTTTGTGACACTGTCAATTATGTTAAGCTCTTCGCTATCAACATTCATCATCGTT 1175
DB 970 TGATTTTGTAACTTGTCCATCGCCATCACCGTCTTCGTGCTCAACGTGCTACAGAA 1029
QY 1176 CTTCTTCAACACATATGCGCGCTTTGGTCGCAAGATATTTCTTTCACACGCTTC 1235
DB 1030 CCCCAGACACACA---CAATGCCCTCATGGTGAAGACTGTATTTCTTGAACCTGCTC 1086
QY 1236 CCAAACTGCTTTGCGCATGAGAATC 1259
DB 1087 CCAGGTCATGTTTCATGACCAGGC 1110

RESULT 11
US-10-349-836-5
; Sequence 5, Application US/10349836
; Publication No. US20030138911A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/349,836
; FILING DATE: 23-Jan-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 07-Jun-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3496 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 232...2115
; OTHER INFORMATION: alpha4 subunit human neuronal
; nicotinic acetylcholine receptor
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-349-836-5

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Query Match      16.6%; Score 303.2; DB 13; Length 3496;
Best Local Similarity 59.3%; Pred. No. 7.5e-71;
Matches 575; Conservative 0; Mismatches 383; Indels 12; Gaps 3;

QY 293 GAAGATAGTTGCTTAAAGGATTTATTTCAAGACTACGAAGATGGTTCGTCCTGTGAA 352
DB 340 GAGGAGCGCTCCTGAAGAACTCTTCCCGGTTACAACAAGTGGTCCGACCGGTGCC 399
QY 353 CACCTGAATGACAAATAAATAAATTTGGACTTGCAATATCTCAATTTGGTGTGATGTG 412
DB 400 AACATCTCGAGCGTGGTCTCGTCGCTTGGCCGTGTCATCGCTCAGCTCATTTGACGTG 459
QY 413 GATGAGAAAAATCAGTTAATGACAAACAAACGCTCGTTGTTGAAACAGGAATGATGATGA 472
DB 460 GATGAGAGAACCAAGATGATGACCAACGAAACGATGCGGTGAACGAGGAGTGGCAGCACTAC 519
QY 473 AAAATTAAGATGGAACCCCTGATGACTATGTTGGAATAAAGTTATACGTGTTCTTCACAC 532
DB 520 AAGCTGCGCTGGGACCCAGCTGACTATGAGAAATGTCACCTCCATCCGATCCCTCCGAG 579
QY 533 TCTGCTCGACACCAAGACATCGTTTGTGATAATGAGATGGACGTTTGAAGGGACC 592
DB 580 CTCATCTGGCGCGGACATGCTCTCTACAAATGCTGACGGGACTTTCGGGTACCC 639
QY 593 AGTACGAAAACAGTCATCAGGTACAAAT---GGCAGCTGTACCTGGACTCCACCGGCAAC 649
DB 640 CACCTGACCAAGGCCACCTGTTCCATGACGGGGGTGAGTGAGTCTCCCGGCCATT 699
QY 650 TACAAAAGTCTGTACCATGATGTCAGTTTTCCTTCCCATTTGACCTTCAGAACTGTGCC 709
DB 700 TACAAGAGCTCTGCGAGATGACGTCACTCTTTCCTCTTCGACGACGAGAACTGTGCC 759
QY 710 ATGAAATTTGTTCTTGTGACTTATGATGATGATGATGATGATGATGATGATGATGATG 769
DB 760 ATGAAATTTGCTCTGACCTTACGAAAGGCAAGATGACCTGGTGAACATGACACAGC 819
QY 770 GATGTAGACAAGAGAGATTTTTTTTGAATATGAGAAATGGGAGATTTGTGAGTGCACAGGG 829
DB 820 CGCGTGGACAGCTGACCTCTCTGGGAGAGTGGGAGTGGTCTATCGTGGACCGCGTGGC 879
QY 830 AGCAAGAAACAGAACCGACGAGCTGTTC-----TGGTATCGGTATGTCTACTTACTCA 883
DB 880 ACCTACAAACACGAGGAGTACGAGTGTGCGCGGAGATCTACCCGACATCACCTATGCC 939
QY 884 TTGTGTAATCAAGCGCTCGCTCTCTTTTATACCTTGTTCCTTATATATACCTGTATTTGG 943
DB 940 TTGTCATCCGCGCGCTCGCGCTCTCTTACACCATCAACCTCATCATCCCTGCTGCTC 999
QY 944 CTCTCATTTTAACTGTACTTGTCTCTCTATCTCTTCAATGAAAGGTGAAAGATTTGT 1003
DB 1000 ATCTCTGCTCACCGTGTGCTGTCTTCTTACCTGCTCGAGTGTGGGAGAGATCAG 1059
QY 1004 CTCTGACTTCAGTACTGTGTGTGTGATGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1063
DB 1060 CTGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1119
QY 1064 CCATCATCTTCAAAAGTACATACCTCTAATTTGGAGATATCTGTTATTTACCATGATTTT 1123
DB 1120 CCGTCCACTCAGTGGTTCATCCCACTCATCGCGAGTACCTGCTGTTTCCACCATGATCTTC 1179
QY 1124 GTGACACTGTCAATATGTAACCGTCTCTGCTATCAATTCATCTCTCTCTCTCTCTCTCTCA 1183
DB 1180 GTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1239
QY 1184 ACACATAAGCATGGCGCTCTTGGTCCGCAAGATATTTCTTCAACAGCTTCCCAAACTG 1243
DB 1240 ACGCACA---CCATGCCACCTGGGTACGAGGGTCTTCTCTGGACATGTCGCCACGCTG 1296
QY 1244 CTTTGTGATGA 1253
DB 1297 CTCCTCATGA 1306
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RESULT 12

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US-09-878-178-1659/c
; Sequence 1659, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secretist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1659
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Homo sapien
; NAME/KEY: misc feature
; LOCATION: (1)...(296)
; OTHER INFORMATION: n = A,T,C or G
US-09-878-178-1659
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Query Match 16.1%; Score 295; DB 10; Length 296;

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Best Local Similarity 99.7%; Pred. No. 2e-69;
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 665 ACCATAGATGTCAGCTTTTCCCATTTGACCTTCAGAACTGTTCCATGAAATTTGGTTCT 724
DB 296 ACCATAGATGTCAGCTTTTCCCATTTGACCTTCAGAACTGTTCCATGAAATTTGGTTCT 237
QY 725 TGGACTTATGATGATCAGGTTGATATATTTCTAGAGGACCAAGATGTAGACAAGAGA 784
DB 236 TGGACTTATGATGATCAGGTTGATATATTTCTAGAGGACCAAGATGTAGACAAGAGA 177
QY 785 GATTTTTTGTATATGAGAAATGGAGATTTGTAGTGCACAGGAGCAAGAGAAACAGA 844
DB 176 GATTTTTTGTATATGAGAAATGGAGATTTGTAGTGCACAGGAGCAAGAGAAACAGA 117
QY 845 ACCGACAGCTGTTCCTGGTATCCGTATGTCATTTACTTACTTGTATTAATCAAGCGCTGCT 904
DB 116 ACCGACAGCTGTTCCTGGTATCCGTATGTCATTTACTTACTTGTATTAATCAAGCGCTGCT 57
QY 905 CTCTTTTATACCTTGTTCCTTTAATACCTGTTATGGGCTCTCATTTTAACTGT 960
DB 56 CTCTTTTATACCTTGTTCCTTTAATAATACCTGTTATGGGCTNTCATTTTAACTGT 1
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RESULT 13

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US-10-046-935-1659/c
; Sequence 1659, Application US/10046935
; Publication No. US20020156011A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secretist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.527C1
; CURRENT APPLICATION NUMBER: US/10/046,935
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 2239
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1659
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 15
; OTHER INFORMATION: n = A,T,C or G
US-10-046-935-1659

Query Match      16.1%; Score 295; DB 14; Length 296;
Best Local Similarity 99.7%; Pred. No. 2e-69;
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 665 ACCATAGATGTCAGGTTTCCCATTTGACCTTCAGAACTGTTCCATGAAATTTGGTTCT 724
DB 296 ACCATAGATGTCAGGTTTCCCATTTGACCTTCAGAACTGTTCCATGAAATTTGGTTCT 237
QY 725 TGGACTTATGATGATCAGAGTTTGATATAATCTAGAGACCAAGATGTAGACAAGAGA 784
DB 236 TGGACTTATGATGATCAGAGTTTGATATAATCTAGAGACCAAGATGTAGACAAGAGA 177
QY 785 GATTTTTTGGTAATGGAGATGGGAGATTGTGAGTGCAACAGGAGCAAAAGGAAACAGA 844
DB 176 GATTTTTTGGTAATGGAGATGGGAGATTGTGAGTGCAACAGGAGCAAAAGGAAACAGA 117
QY 845 ACCGACAGCTGTGCTGGTATCGGTATGTCACCTTCACTTCTCACTTCTCACTTCTCACTTCT 904
DB 116 ACCGACAGCTGTGCTGGTATCGGTATGTCACCTTCACTTCTCACTTCTCACTTCTCACTTCT 57
QY 905 CTCCTTTTATACCTTGTTCCTTATAATACCTGTATGGGCTCTCATTTTAACTGT 960
DB 56 CTCCTTTTATACCTTGTTCCTTATAATACCTGTATGGGCTCTCATTTTAACTGT 1

RESULT 14
US-10-146-502-1659/c
; Sequence 1659, Application US/10146502
; Publication No. US20030069180A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secret, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Scolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121-527C2
; CURRENT APPLICATION NUMBER: US/10/146,502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1659
; LENGTH: 296
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 15
; OTHER INFORMATION: n = A,T,C or G
US-10-146-502-1659
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Query Match      16.1%; Score 295; DB 15; Length 296;
Best Local Similarity 99.7%; Pred. No. 2e-69;
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 665 ACCATAGATGTCAGGTTTCCCATTTGACCTTCAGAACTGTTCCATGAAATTTGGTTCT 724
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QY 725 TGGACTTATGATGATCAGAGTTTGATATAATCTAGAGACCAAGATGTAGACAAGAGA 784
DB 236 TGGACTTATGATGATCAGAGTTTGATATAATCTAGAGACCAAGATGTAGACAAGAGA 177
QY 785 GATTTTTTGGTAATGGAGATGGGAGATTGTGAGTGCAACAGGAGCAAAAGGAAACAGA 844
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QY 845 ACCGACAGCTGTGCTGGTATCGGTATGTCACCTTCACTTCTCACTTCTCACTTCTCACTTCT 904
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DB 56 CTCCTTTTATACCTTGTTCCTTATAATACCTGTATGGGCTCTCATTTTAACTGT 1

RESULT 15
US-10-157-031-27
; Sequence 27, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-157-031-27
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Query Match      16.1%; Score 294.4; DB 15; Length 1667;
Best Local Similarity 58.9%; Pred. No. 1.1e-68;
Matches 568; Conservative 0; Mismatches 381; Indels 15; Gaps 3;

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QY 348 TGAACACCTGTAATGACAAATAATAATAATTTTGGACTTGGCAATATCTCAATTTGGTGG 407
DB 173 TGAAGACACCGCCAGGTCGTGGAGGTCACCGTGGGCGCTGCAGCTGTGATACAGCTCATCA 232
QY 408 ATCTGGATGAGAAATAATCAAGTTAATGACAAACAAACGCTCTGTTTGAACAGGAATGATAG 467
DB 233 ATGTGATGAAGTAATCAGATCGTGACAAACCAATGTGCGTCTGAAACAGCAATGGGTGG 292
QY 468 ATGTTAAATTAAGATGGAAACCCCTGATGACTATGGTGGAAATAAAAGTTATACGTTTCCCTT 527
DB 293 ATTACAACTTAATATGGAATCCAGATGACTATGGCGGTGTGAAAAAATTCACATTTCCTT 352
QY 528 CAGACTCTCTCTGGACACAGACATCGTTTGTGTTGATTAATGAGATGAGACGTTTGGTGGT 584
DB 353 CAGAAAGATCTGGCGCCAGACCTTGTCTCTATAACAATGCAGATGGTGTGACTTTTGCTA 412
QY 585 AAGGACACAGTACGAAACAGTCATCAGTCAATGGCACTGTCACTCGACTCCACCGG 644
DB 413 TTGTCAAGTTCCACAAAGTGTCTCTGACGTACATGCGCCACATCAGTGGACACCTCCAG 472
QY 645 CAAACTACAAAAAGTTCTCTGATACATAGATGTCAACGTTTTTCCCATTTTGACCTTCAGAACT 704
DB 473 CCATCTTTAAAGCTACTGTGAGATCATCGTCAACCCACTTTCCCTTTGATGAACAGACT 532
QY 705 GTTCCATGAAATTTGGTCTTGGACTTATGATGGATTCACAGGTTGATATAATTTCTAGAGG 764
DB 533 GCAGCATGAAGCTGGGCACCTGAGACCTAGACGGCTCTGTCTGTTGGCCATCAACCCGAAA 592
QY 765 ACCAGATGTAGCAAGAGAGATTTTTTTTGAATAATGGAGAAATGGGAGATTTGTGAGTGCA 824
DB 593 GCGACCAAGCCAGCTTCAGCAACTTCATGGAGAGCGGGGAGTGGGTGATCAAGAGTCCC 652
QY 825 CAGGGAGCAAGGAAACAGAACCGACAGCTGTTG-----CTGGTATCCGTATGTCA 875
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Db	653	GGGGCTGGAGCACTCCGTGACCTATTCCTGTCGCCGACACCCCTACCTGGACATCA	712
Qy	876	CTTACTCATTTGTAATCAAGCGCCTGCTCTCTTTTATACCTTGTTCCTTATAATACCCCT	935
Db	713	CCTACCACCTTCGTATGACGCGCCTGCCCTCTACTTCATCGTCAACGTCACTATCCCT	772
Qy	936	GTAATTGGGCTCTCATTTTAACTGTACTGTCTTCTATCTTCCTTCAAAATGAAGTGAAA	995
Db	773	GCCTGCTCTTCTCTCTTCTTAACTGGCCTGGTATTCTACCTGCCACAGACTCAGGGGAGA	832
Qy	996	AGATTGTCTCTGCACTTCAGTACTTGTCTCTTGTGACTGTCTCTCTTCTGGTTATTGAAG	1055
Db	833	AGATGACTCTGAGCATCTCTGCTTACTGTCTTGTGACTGTCTCTCTCTGGTCATCGTGG	892
Qy	1056	AGATCATACCATCATCTTCAAAAGTCATACCTCTAAATTGGAGAGTATCTGGTATTACCA	1115
Db	893	AGCTGATCCCTCCACGTCAGTGTGTCCTCTGATTGGAAATACATGCTGTTACCA	952
Qy	1116	TGATTTTGTGACACTGTCAATATGGTAAACCGTCTTCGCTATCAACATTCATATCGTT	1175
Db	953	TGGTGTGCTCATTTGCTCCATCATCATCTGTCTCATCAACACACACACCCCGCT	1012
Qy	1176	CTTCCTCAACATATGCCATGGCGCCTTTGGTCGGCAAGATATTCTTACACGCTTC	1235
Db	1013	CACCCAGCACCC---ATGTATGCCCACTGGGTGCGGAAGGTTTTTATCGACACTATCC	1069
Qy	1236	CCAA	1239
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC
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Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1828	100.0	1828	4	US-08-487-596-7
2	1828	100.0	1828	4	US-08-660-451A-7
3	557.6	30.5	1925	4	US-08-660-451A-15
4	554.2	30.3	1927	4	US-08-487-596-15
5	554.2	30.3	1927	4	US-08-484-722-3
6	334.6	18.3	2277	1	US-08-496-855A-1
7	334.6	18.3	2277	4	US-08-487-596-1
8	334.6	18.3	2664	4	US-08-660-451A-1
9	324.8	17.8	2068	2	US-08-466-589-1
10	324.8	17.8	2068	3	US-08-700-636-1
11	324.8	17.8	2068	4	US-08-467-574-1
12	324.8	17.8	2068	4	US-09-217-345-1
13	315.6	17.3	1908	4	US-08-660-451A-3
14	314.8	17.2	1743	4	US-08-466-589-9
15	314.8	17.2	1743	4	US-08-484-722-1
16	314.8	17.2	1743	4	US-08-660-451A-9
17	308.8	16.9	1756	2	US-08-466-589-3
18	308.8	16.9	1756	2	US-08-700-636-3
19	308.8	16.9	1756	3	US-08-467-574-3
20	308.8	16.9	1756	4	US-09-217-345-3
21	303.6	16.6	1654	4	US-08-487-596-3
22	303.2	16.6	3496	4	US-08-660-451A-5
23	291.4	15.9	1350	3	US-08-462-351-1
24	291.4	15.9	1350	4	US-09-602-807-1
25	290.4	15.9	2363	4	US-08-487-596-5
26	285.2	15.6	2374	2	US-08-466-589-5
27	285.2	15.6	2374	2	US-08-700-636-5

28	285.2	15.6	2374	3	US-08-467-574-5	Sequence 5, Appli
29	285.2	15.6	2374	4	US-09-217-345-5	Sequence 5, Appli
30	283.4	15.5	1350	6	5468481-2	Patent No. 5468481
31	270.6	14.8	1698	4	US-08-660-451A-19	Sequence 19, Appl
32	268	14.7	1356	6	5194425-2	Patent No. 5194425
33	239	13.1	1521	1	US-08-496-855A-3	Sequence 3, Appli
34	239	13.1	1521	2	US-07-938-154-9	Sequence 9, Appli
35	239	13.1	1521	5	PCT-US91-02311-9	Sequence 9, Appli
36	237.4	13.0	2448	4	US-08-487-596-13	Sequence 13, Appl
37	237.4	13.0	2448	4	US-08-660-451A-13	Sequence 13, Appl
38	237.4	13.0	2450	2	US-08-466-589-9	Sequence 9, Appli
39	237.4	13.0	2450	2	US-08-700-636-9	Sequence 9, Appli
40	237.4	13.0	2450	3	US-08-467-574-9	Sequence 9, Appli
41	237.4	13.0	2450	4	US-09-217-345-9	Sequence 9, Appli
42	237.2	13.0	1915	4	US-08-487-596-17	Sequence 17, Appl
43	237.2	13.0	1915	4	US-08-660-451A-17	Sequence 17, Appl
44	236.8	13.0	1915	1	US-08-496-855A-5	Sequence 5, Appli
45	236.8	13.0	1915	2	US-08-466-589-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-487-596-7
; Sequence 7, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Eliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,596
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO US94/02447
; FILING DATE: 08-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,154
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062

; GENERAL INFORMATION:
 ; APPLICANT: Elliott, Kathryn J.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/660,451A
 ; FILING DATE: June 7, 1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/484,722
 ; FILING DATE: 06/07/95
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 6362-9370B
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-238-0999
 ; TELEFAX: 619-238-0062
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1828 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Genomic DNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 155..1561
 ; OTHER INFORMATION: alpha5 subunit human neuronal
 ; NAME/KEY: 5'UTR
 ; LOCATION: 1...154
 ; OTHER INFORMATION:
 ; NAME/KEY: 3'UTR
 ; LOCATION: 1562...1828
 ; OTHER INFORMATION:
 ; US-08-660-451A-7
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 ; Query Match 100.0%; Score 1828; DB 4; Length 1828;
 ; Best Local Similarity 100.0%; Pred. No. 0;
 ; Matches 1828; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 ; 121 GCGGCTGCCGCGGTTCGCCGCGGCGGCGGCGGTGCGGCGGCGGTGCGGCGGCGG 180
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 1261 TGTAGACAGGTACTTCTCACTCAGAAAGAGGAACTGAGAGTGGTAGTGGACCAAAATCTTC 1320

Db 647 ATTTGATCAATGAAATGTCACAGAAAAGACTTCTTCGATACGGAGAATGGAAATA 706
QY 815 GTGAGTGCAACAGGAGCAAAAGAAACAGAACCGAGCTGTGTGGTATCCGTATGTC 874
Db 707 CTGAATGCAAGGGGATGAAGGGGAACAGAGGAGCGGTGACTCTCTATCCCTTATC 766
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QY 935 TGTATTTGGCTCTCATTTTAACTGTACTGTCTCTCTATCTCTTCAATGAAGTGAA 994
Db 827 TGCTGGGGCTGCTTCTCTACAGTCTTGTTGTTCTATTTACCTTCGATGAGAGAA 886
QY 995 AAGATTTGTCTGCACTTCAGTACTGTGTCTTTGACTGTCTCTCTCTCTGTTATGAA 1054
Db 887 AAATTTTCATTATCCACATCGCTTGGTTTCTCTGACAGTTTCTCTTTAGTGA 946
QY 1055 GAGATCATCATCTCTCAAAAGTCATCTCTAAATGGAGAGTATCTGTATTTACC 1114
Db 947 GAAATCATCCCATGCTCTTCCAAAGTCATCTCTCATTTGGAGAGTACCTGCTGTTCATC 1006
QY 1115 ATGATTTTGTGACACTGTCAATTTATGTAACCGTCTTCGCTATCAACATTCATCATGT 1174
Db 1007 ATGATTTTGTGACCTGCTCTCAATGTTTACCGTGTGTTGCTATTAACGTTCCACAGA 1066
QY 1175 TCTTCTCAACATATGCAATGCAATGCGCTTTGGTCCGCAAGATATTTCTTCCACGCTT 1234
Db 1067 TCTTCTCCAGTACCAACCCATGCGCCCTGGTTAAGAGCTCTTCTGCAAGAACTT 1126
QY 1235 CCAAACTGCTTTGATGAGAGTCAATGTAGACAGTACT----- 1274
Db 1127 CAAAATTTACTTTGATGAAAGATCATGTGATCGCTACTCATCCCGAGAGAGGAG 1186
QY 1275 -----TCACTCAGAAAGAGAACTGAGAGTGTAGT 1306
Db 1187 AGTCAACAGTAGTGAAGGCAAGTCTCGAAGAAAGAAACAGAAACAGCTTAGTGTAT 1246
QY 1307 GGACCAAAATCTTTAGAAACACATTTGGAAGTGGCTCAATTTCTATTGCTTACATTA 1366
Db 1247 GGAGAAAGTTCTAGTTGCTTTTGGAAAGCTGCTGATTCATTAGATACATTTCC 1306
QY 1367 AGACATCATGAAGGAAATGATGTCGTGAGGTTTGAAGATGGAATTCATAGCC 1426
Db 1307 AGACATGTGAGAAAGAAACATTTTATCAGCCAGGTAGTACAGACTGGAAATTTTAGCT 1366
QY 1427 CAGGTTCTGTGCGATGTTCTGTTGAGTCTTTCTTTCTCAATTTGTTGATCTCTT 1486
Db 1367 CAAGTTCTGTGACGAATCTTCTGTTGCTCTTTCTGATGTTGCTAGTACAGCAAGGCTCGGT 1426
QY 1487 GGGCTTTTGTCTCTGTTATTTATATAATGGGCAATA 1523
Db 1427 CTGATTTTACCCTGCTTTGAGATGTTGGCTACATA 1463

RESULT 6

US-08-496-855A-1
; Sequence 1, Application US/08496855A
; Patent No. 5801232
; GENERAL INFORMATION:
; APPLICANT: Eliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,855A
FILING DATE: 20-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9369B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 166..1755
US-08-496-855A-1

Query Match 18.3%; Score 334.6; DB 1; Length 2277;
Best Local Similarity 61.3%; Pred. No. 2.2e-78;
Matches 595; Conservative 0; Mismatches 364; Indels 12; Gaps 3;
QY 292 TGAAGATAGTTTGTCTAAGGATTTTATTTCAAGACTACGAAAGATGGGTTCGTCTGTGGA 351
Db 339 TGAGACCGGCTCTTCAACACCTCTTCGCGGGCTACAAACCGTGGCGCGCCGGTGCC 398
QY 352 ACACCTGAATGACAAATAAATAATTTGGACTTGCATATCTCAATTTGGTGGATGT 411
Db 399 CAACACTTCAGACGTGGTGTGTTGGCTTTGGACTGTCCATCGCTCAGCTCATCGATGT 458
QY 412 GGATGAGAAATCAGTTTAAATGACAAACAAAGCTCTGGTTGAAACAGGAATGATAGATGT 471
Db 459 GGATGAGAAACAAATGATGACCAACCACTCTGGCTAAACAGGAGTGGAGGACTA 518
QY 472 AAAATTAAGATGGAACCTCTGATGACTATGTGGGAATAAAGTTATACGTGTTCTTTCAGA 531
Db 519 CAAACTGCGCTGGAACCCCGCTGATTTTGGCAACATCATCATCTCTCAGGGTCCCTTCTGA 578
QY 532 CTCTGTCTGGACACAGACATCGTTTGTGTAATGACAGATGACGCTTTTGAAGGAC 591
Db 579 GATGATCTGGATCCCGACATTTCTCTACAAACATGACAGATGGGAGTTTGCAGTGAC 638
QY 592 ---CAGTACGAAACAGTTCATCAGGTACATGGCACTGTACCTGGACTCCACCGGCAAA 648
Db 639 CCACATGACCAAGGCCACCTCTTCTCCACGGGCACTGTGCACTGGGTGCCCCCGCCAT 698
QY 649 CTACAAAAGTTCTCTGATACATAGATGTACCGTTTTCCTTTCACCTTCAGAACTGTTC 708
Db 699 CTACAGAGCTCTCTCGAGCATCGACGTCACCTCTTCTCCCTTCGACAGAGACTGCA 758
QY 709 CATGAAATTTGGTCTTGGACTTATGATGGAATCAGGTTGATATAATTTAGAGGACA 768
Db 759 GATGAAATTTGGCTCTCTGGAATTATGACAGGCCCAAGATCGACCTGGAGCAGATGGAGCA 818
QY 769 AGATGTAGACAGAGATTTTGTATGATGAGAGATGGGAGATTTGTGAGTGAACAGG 828
Db 819 GACTGTGAGCTGAAGGACTACTGGGAGAGCGGAGTGGGCCATCGTCAATGCCACGG 878

Db 1568 CGTCACCTGTCCATCGTCATCACCGCTTCCTGGTCTCAATGTGCAACACCGCTCCCCAG 1627
Qy 1183 AACACATAATGCCATGGCGCTTGGTCCGCAAGATATTTCTTACACGCTTCCAACT 1242
Db 1628 CACCACA---CATGCCCACTGGGTGCGGGGGGCCCTTCTGGGCTGTGTGCCCCGGTG 1684
Qy 1243 GCTTTGCATGA 1253
Db 1685 GCTTCTGATGA 1695

RESULT 9

US-08-466-589-1
; Sequence 1, Application US/08466589
; Patent No. 5837489
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,589
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9950
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2068 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 166..1752
; US-08-466-589-1

Query Match 17.8%; Score 324.8; DB 2; Length 2068;
Best Local Similarity 59.9%; Pred. No. 7.9e-76;
Matches 580; Conservative 0; Mismatches 379; Indels 9; Gaps 2;
Qy 292 TGAAGATAGTTTCTTAAAGATTTTATTTCAAGACTACGAAGATGGGTTCCTCTGTGGA 351
Db 339 TGAGGACCGGCTCTTCAACACCTCTTCCGGGGCTACACCGCTGGCGCGCGCGGTGCC 398
Qy 352 ACACCTGAATACAAAATAAAATTTGGACTTGGCATATCTCAATTTGGTGGATGT 411
Db 399 CAACACTTCAGACGTGGTGTGTTGGCGCTTGGACTGTCCATCGCTCAGCTCATCGATG 458

Qy 412 GGATGAGAAAAATACGTTAATGACAAACAAACGCTGTGGTTGAAACAGGAATGGATAGATGT 471
Db 459 GGATGAGAAAGAACCAAAATGATGACCAACAAACGCTGTGGTTGAAACAGGAATGGAGCGCA 518
Qy 472 AAAATTAGATGGAAACCTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 531
Db 519 CAAACTGCGCTGGAAACCGCGCTGATTTTGGCAACATCACTCTCTCAGGGTCCCTTCTGA 578
Qy 532 CTCTGTCTGGACACCAAGACATCGTTTGTGATGATGATGATGATGATGATGATGATGATG 591
Db 579 GATGATCTGGATCCCGACATTTGTTCTTACAACAANNTGGGAGTTTGCAGTGACCCA 638
Qy 592 CAGTACGAAAAAGTCAATGAGTACAAATGGCACTGTCACTGGACTTCCACCGGCAAACTA 651
Db 639 CATGACCAAGGCCACCTCTTCTCCACGGGCACTGTGCACTGGGTGCCCGGCCACTCTA 698
Qy 652 CAAAAGTTCTGTACCATAGATGTACAGTTTTCCTTCCATTTGACCTTCAGAACTGTTCCAT 711
Db 699 CAAGAGCTCTCGACATCGACGTCACTTCTTCCCTTCGACCAAGTCAAGAT 758
Qy 712 GAAATTTGGTCTTGGACTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 771
Db 759 GAAGTTTGGCTCTGGACTTATGACAGCCCAAGATCGACCTGGAGCAGATGGAGGAGAC 818
Qy 772 TGTAGACAAAGAGATTTTTTTTATTAATGGAGATGGAGATTTGTGAGTGCACAGGGAG 831
Db 819 TGTGGACCTGAAGGACTACTTGGAGAGCGCGGAGTGGGCGCATCGTCAATGCCACGGGCAC 878
Qy 832 CAAAGGAAACAGAACCGACAGCTGTTGC-----TGGTATCCGTATGTCACTTACTTACT 885
Db 879 CTACAAACAGCAAGAAAGTACGACTGTGTCGCCCGAGATCTTACCCCGAGCTCACCTACG 938
Qy 886 TGTAAATCAAGCGCTGCTCTCTTTTATATACCTTTGTTCTTATAATACCTGTATTTGGGCT 945
Db 939 CGTATCCCGGGCTGCGGCTCTTCTACACCATCAACCTCATCATCTCCCTGCTGCTCAT 998
Qy 946 CTCATTTTAACTGTACTTGTCTTCTATCTTCTTCAAAATGAAGGTGAAAAGATTTGTCT 1005
Db 999 CTCCTGCCCTCACTGTGCTGTCTTCTTACCTGCCCTCCGACTGCGGCGAGAAGATCACGCT 1058
Qy 1006 CTGCACTTCACTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 1065
Db 1059 GTGCAATTCGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 1118
Qy 1066 ATCATCTTCAAAAGTCACTACCTCTTAATGGAGATATCTGGTATTTTACCATGATTTTGT 1125
Db 1119 GTCCACTCGTGGTGTATCCCGCTCATCGCGAGTACCTGTGCTTCCATCATGATCTTGT 1178
Qy 1126 GACACTGTCAATTAATGTAACCGCTTTCGCTATCAACATTCATCATCTTCTTCTCAAC 1185
Db 1179 CACCTGTCCATGCTCATCACCGCTTTCGCTCATATGTTGGACCAACCGCTCCCGCAGCAC 1238
Qy 1186 ACATAATGCAATGGCGGCTTGTGTCGCAAGATATTTCTTACACGCTTCCCAAACTGCT 1245
Db 1239 CCACA---CCATGCCCACTGCGGTGGGGGGGCCCTTCTTGGGCTGTGTGCCCGGGCT 1295
Qy 1246 TTGCATGA 1253
Db 1296 TGTGATGA 1303

RESULT 10

US-08-700-636-1
; Sequence 1, Application US/08700636
; Patent No. 5910582
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/700,636

FILING DATE: 16-JUL-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/028,031

FILING DATE: 08-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Reiter, Stephen E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 9368

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-546-4737

TELEFAX: 619-546-9392

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2068 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: both

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 166...1752

US-08-700-636-1

Query Match 17.8%; Score 324.8; DB 2; Length 2068;

Best Local Similarity 59.9%; Pred. No. 7.9e-76;

Matches 580; Conservative 0; Mismatches 379; Indels 9; Gaps 2;

QY	292	TGAAGATAGTTGCTTAAAGATTTATTTCAAGACTACGAAAGATGGTTCGCTGTGGA	351
DB	339	TGAGGACCGGCTTTCAAAACACCTCTCGGGGCTACAAACCGCTGGGGCGCCCGGTC	398
QY	352	ACACCTGAATGACAAATAAATAATTTGGACTTGCAATATCTCAATTGGTGGATGT	411
DB	399	CAACACTTCAGACGTGGTGAATTTGGGCTTTGGACTGTCCTCAGCTCAGCTCATCGATG	458
QY	412	GGATGAGAAATATCAGTTAATGACAAACAAACGCTCTGGTTGAAACAGGAATGGATAGATGT	471
DB	459	GGATGAGAAAGAACCAATGATGACCAACCAACGCTCTGGCTTAAACAGGAGTGAGGACTA	518
QY	472	AAATTAATGATGAAACCTGATGACTATGTTGGAAATAAAGTTATACGTTCCTTCAGA	531
DB	519	CAAACTGGCTGGAACCCCGCTGATTTGGCAACATCATCTCTCAGGGTCCCTCTGA	578
QY	532	CTCTCTGGACACGACATCGTTTGTGTTGATATGACATGACGACCTTTTGAAGGAC	591
DB	579	GATGATCTGGATCCCCGCAATGTTCTCTACAAACAAANNATGGGAGTTTGACGTGACCCA	638
QY	592	CAGTACGAAAAACAGTCATCAGGTACAAATGGCACTGTCCACTGGACTCCACCGGCAAACTA	651
DB	639	CATGACCAAGGCCACCTCTTCTCAACGGGCACTGTGCACTGGTGGCCCGGCATCTA	698
QY	652	CAAAAGTTCCTGTACATAGATGTCAAGTTTTCCTCAATTTGACCTTCAGAACTGTTCCAT	711
DB	699	CAAGAGCTCTCAGCATCGACCTCACCTTCTTCCCTTCGACCAAGCAAGTCAAGAT	758
QY	712	GAAATTTGGTCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	771
DB	759	GAAATTTGGTCTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	818

QY	772	TGTAGACAAGAGAGATTTTTTTTGTATATGAGAAATGGAGAGATTTGTAGTCAACAGGAG	831
DB	819	TGTGACCTGAAGGACTACTGGAGAGCGGAGTGGGCCATCGTCAATGCCACCGGCAC	878
QY	832	CAAGGAAACAGAACCGACAGCTGTGC-----TGGTATCGGTATGTCACTTACTT	885
DB	879	CTACAAACAGCAAGAGTACGACTGCTGCGCGAGATCTACCCCGACGTCACCTAGCCTT	938
QY	886	TGTAATCAAGCGCTGCTCTCTTTTATPACCTTGTTCCTTATAATPACCTGTATTGGGCT	945
DB	939	CGTCATCGGCGGCTGCGCTCTTTTACACCATCAACCTCATCATCCCTGCTGCTCAT	998
QY	946	CTCATTTTAACTGATCTTGTCTTCTATCTTCTTCAAAATGAAGTGAAGATTTGTCT	1005
DB	999	CTCCTGCTCACTGTGCTGTCTTCTACCTGCCCTCGACTGCGCGGAGAAAGATCACGCT	1058
QY	1006	CTGCACTTCAGTACTGTGCTCTTGTGACTGTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1065
DB	1059	GTGCATTTGCGTGTGCTGTCACTCACCGCTTCTTCTGCTGTCTCATCTGAGATCATCCC	1118
QY	1066	ATCATCTTCAAAAGTCATACCTCTAAATGGAGAGATCTGCTTATTTTACCATGATTTTGT	1125
DB	1119	GTCCACCTGCTGTGCTCATCCGCTCATCGGAGTACTGCTGTTCACCATGATCTTGT	1178
QY	1126	GACACTGTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1185
DB	1179	CACCTGTGCTCATCGTCACTCACCGCTTCTGCTCAATGTGAGCAACCGCTCCCGCAGC	1238
QY	1186	ACATAATGCCATGGGCTTGTGTCGCGAGATATTTCTTCAACAGCTTCCCAAACTGCT	1245
DB	1239	CCACA---CCATGCCCACTGGGTGCGGGGGGCGCTTCTTGGGCTGTGTGTCGCTTGG	1295
QY	1246	TGTCATGA 1253	
DB	1296	TCTGATGA 1303	

RESULT 11

US-08-467-574-1

Sequence 1, Application US/08467574

Patent No. 6022704

GENERAL INFORMATION:

APPLICANT: Elliot, Kathryn J.

APPLICANT: Ellis, Steven B.

APPLICANT: Harpold, Michael M.

TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE

TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClaim

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,574

FILING DATE: June 5, 1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/028,031

FILING DATE: March 8, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L

REGISTRATION NUMBER: 33,779

REFERENCE/DOCKET NUMBER: 6362-9949

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-238-0999

TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2068 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 166..1752
US-08-467-574-1

Query Match 17.8%; Score 324.8; DB 3; Length 2068;
Best Local Similarity 59.9%; Pred. No. 7.9e-76;
Matches 580; Conservative 0; Mismatches 379; Indels 9; Gaps 2;

292 TGAAGATAGTTGCTTAAGGATTTATTTCAAGACTACGAAGATGGGTTCTGCTCTGGGA 351
Db |||||
339 TGAGGACCGGCTCTTCAACACCTCTTCGGGGCTACACCGCTGGCGCGCCGGTGCC 398
Qy |||||
352 ACACCTGAATGACAAATAAAATTTGGACTTGCATATCTCAATGGTGGATGT 411
Db |||||
399 CAACACTTCAGACGTGGTGTGTTGGCGCTTTGGACTGTCCATCGCTCAGCTCATCGATGT 458
Qy |||||
412 GGATGAGAAAATCAGTTAATGACAAACAAACGCTGCTGTTGAAACAGGAATGGATAGATGT 471
Db |||||
459 GGATGAGAGAACCAATGATGACCAACAGCTGCTGCTTAACAGAGATGGAGCGACTA 518
Qy |||||
472 AAAATTGAATGGAACCTGATGACTATGTTGGAAATAAAAGTTATACGTTCTCTTCAGA 531
Db |||||
519 CAAACTCGCTGGAACCCCGCTGATTTTGGCAACATCACATCTCTCAGGCTCCCTCTGA 578
Qy |||||
532 CTCTGCTGACACCAACATCGTTTGTGTAATGACAGATGGAGCTTTTGAAGGAC 591
Db |||||
579 GATGATCTGATCCCGACATTTGTTCTTCAACAAANNTGGGAGTTTCAGTGAACCA 638
Qy |||||
592 CAGTACGAAACAGTCAATCAGGTACATGACCTGCTCAGCTGACCTCCACCGGCAACTA 651
Db |||||
639 CATGACCAAGGCCACCTCTTCCACGGGACATGTCATGGTGGCCCGCGGCATCTA 698
Qy |||||
652 CAAAGTTCCTGTACCATAGATGTCAGCTTTTCCCAATTTGACCTTCAGAACTGTTCCAT 711
Db |||||
699 CAAGAGCTCTGACGATGACGCTCCTCTTCCCTTCGACCAAGCAAGTCAAGAT 758
Qy |||||
712 GAAATTTGGTCTTGGACTATGATGATGATCAGAGTTGATATAATTTAGAGGACAGA 771
Db |||||
759 GAAGTTTGGCTCTGAGCTTATGACAGGCGCAAGATCGACCTGGAGCAGATGGAGCAGAC 818
Qy |||||
772 TGTAACAAGAGATTTTGTGATAATGGAGATGGAGATGCTGAGTCAACAGGGAG 831
Db |||||
819 TGTGGACTGAGGACTACTGGGAGCGGAGTGGGCATCTCAATGCCAGGGCAC 878
Qy |||||
832 CAAAGGAAACAGAACCGACAGCTGTC-----TGGTATCCGATGTCATCTACTCAT 885
Db |||||
879 CTACAACAGCAAGATGACGACTGCTGGCGGAGATCTACCCGACGCTACCTAGGCTT 938
Qy |||||
886 TGTAAATCAAGCGCTGCTCTTTTATACCTGTTCTTTATATACCTGATTTGGGCT 945
Db |||||
939 CGTCACTCGGCGGCTGCGGCTCTTCTACACCATCAACCTCATCATCCCTGCTGCTCAT 998
Qy |||||
946 CTCAATTTTAACTGCTACTGCTCTATCTCTCTTCAATCAAGTCAAGATTTTGTCT 1005
Db |||||
999 CTCCTGCTCACTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1058
Qy |||||
1006 CTGCACTTCAGTACTTGTGCTTTGACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1065
Db |||||
1059 GTGCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1118
Qy |||||
1066 ATCATCTTCAAAAGTCATACCTCTAAATTTGAGAGATGATCTGATTTACCATGATTTTGT 1125
Db |||||
1119 GTCCACCTCGTGTGCTATCCGCTCATCCGCGAGTACCTGCTGTTTCCACCATGATCTTCTGT 1178

465	Qy	TAGATGTAAATTAAGATGGAAACCTGATGACATATGGTGGAAATAAAGTTATACGTGTTC	524
466			
461	Db	ATGACTACAAGCTGAAGTGGAAACCCCTCTGACTATGGTGGGCAGAGTTTCATCGGTGTC	520
462			
525	Qy	CTTCAGACTCTGCTGCACACAGACATCGTTTTTTGTATATATGACAGATGGACGTTTTG	584
526			
521	Db	CTGCACAGAAGATCTGGACCGCAGACATGTGCTGTATAAATGCTGTTGGGGATTTC	580
522			
585	Qy	AAGGG---ACCAGTACGAAACACAGTCAATAGGACATGTGCACCTGGACTCCAC	641
586			
581	Db	AGGTGGACGACAGACCAAAGCCCTTACTCAAGTACACTGGGGAGGTGACTTGGATACCTC	640
582			
642	Qy	CGGCAAACTACAAAAGTTCTGTACCATAGATGTCAGCTTTTCCCATTTGACCTTCAGA	701
643			
641	Db	CGGCCATCTTTTAGAGCTCTCTGTAAAATCGACGTGACCTACTTCCCGTTTGAATTACCAA	700
642			
702	Qy	ACTGTTCCATGAATTTGGTTCTTTGGACTTATGATGGATCACAGGTGTGATATAATTCTAG	761
703			
701	Db	ACTGTACCATGAGTTCCGTTCTTGCTCTACGNTAAGCGAAATCGATCTGGTCTGTA	760
702			
762	Qy	AGGACCAAGATGTAGACAAGAGAGATTTTTTTGATAATGGAGAAATGGAGATGTGAGTG	821
763			
761	Db	TCGGCTCTTCATGAACCTCAAGGACTATTGGGAGAGCGCGAGTGGGCCCATCATCAAG	820
762			
822	Qy	CACACGGGCAAGGAAACAGACACGACGCTGTTGCTGG-----TATCCGTATGTCA	875
823			
821	Db	CCCAGGCTACAAACACGACATCAAGTACAACTGCTCGCAGGAGATCTACCCGACATCA	880
822			
876	Qy	CTTACTCATTTGTAATCAAGCGCGCTGCTCTCTTTTATACCTTGTTCCTTTATAATACCTT	935
877			
881	Db	CATACTCGCTGTACATCCGGCGCTGCCCTTGTTCTACACCATCAACCTCATCCCT	940
882			
936	Qy	GTATTGGGCTCTCATTTTTTAACGTGACTTGTCTTCTATCTTCTCTTCAAATGAAGTGAAA	995
937			
941	Db	GCCTGTCTCATCTCCTCTCCTCACTGTGCTGCTTCTTCTACCTGCCCTCGACTCGGGTGAGA	1000
942			
996	Qy	AGATTTGCTCTGCACATTCACTCTGTGCTTTTGACTGTCTTCTTCTGTTATTGGAAG	1055
997			
1001	Db	AGGTGACCTGTGCATTTCTGTCTCTCTCCCTGACGGTGTCTCTCGTGATCACTG	1060
1002			
1056	Qy	AGATCATACCATCATCTTCAAAGTCATACCTCTAAATTGGAGAGTATCTCGGTATTTACCA	1115
1057			
1061	Db	AGACCATCCCTTCCACCTCGCTGGTCAATCCCCCTGATTGGAGAGTACCTCCTGTTACCA	1120
1062			
1116	Qy	TGATTTTGTGCACACTGTGCAATTATGGTACACCGTCTTCGCTATCAACATTCATCATCGTT	1175
1117			
1121	Db	TGATTTTGTGAACCTTGTTCATGTTCATACCGGCTTTCGTCCTCAACGTGCACCTACAGAA	1180
1122			
1176	Qy	CTTCTCTCAACACATAAATGCCATGGCGCTTTGGTCCGCAAGATATTCTTTCACACGCTTC	1235
1177			
1181	Db	CCCCGACGACACA---CAATGCCCTCATGGGTGAGACTGTGATTCTTGAACCTGCTCC	1237
1182			
1236	Qy	CCAAACTGCTTTGCATGAGAAGTC	1259
1237			
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1239			

RESULT 14

RESOL 14
US-08-487-596-9

US-08-487-396-5
: Sequence 9, Application US/08487596; sequence 3, Application No. 6440681
; Patent No. 6440681

; GENERAL INFORMATION:

APPLICANT: Elliot, Kathryn J.

APPLICANT: Ellis, Steven B.

APPLICANT: Harpold, Michael M

1. TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND

; TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL

; TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street
CITY: San Diego

; CITY: San Diego

```

STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,596
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1743 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 143..1627
OTHER INFORMATION: /product= "ALPHA-6 SUBUNIT"
US-08-487-596-9

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Query Match 17.2%: Score 314.8; DB 4; Length 1743;

Query Match	17.2%	Score 314.8; DB 4
Best Local Similarity	59.6%	Pred. No. 3.2e-73;

Matches 589; Conservative 0; Mismatches 387; Indels 12; Gaps 3;
BEST LOCAL SIMILARITY 55.8%; FREQ. NO: 3.2E-73;

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Qy	352	ACACCTGAATGCACAAAATAAAATTTGGACTTTGGCAATATCTCAATTTGGTGGGATGT	411
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Db	481	TAAGATTTGGAAGCCCGACATTGTTCTCTATAACAAATGCTGTTGGTGNACTTCCAAGTAGA	540
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RESULT 15

RESULT 13
 US-08-484-722-1
 ; Sequence 1, Application US/08484722
 ; Patent No. 6485967
 ; GENERAL INFORMATION:
 ; APPLICANT: Elliott, Kathryn J.
 ; APPLICANT: Harpold, Michael M.
 ; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
 ; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,722
 ; FILING DATE:
 ; CLASSIFICATION: 435

[illegible]

Search completed: December 23, 2003, 15:38:12
Job time : 131 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 23, 2003, 15:35:43 ; Search time 523 Seconds
(without alignments)
9435.129 Million cell updates/sec

Title: US-09-703-951A-7

Perfect score: 1828

Sequence: 1 CCCGCGGAGACTGGCGC.....ATCTAGTATTGTATCTCTGG 1828

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1828	100.0	1828	18	Neuronal nicotinic
2	1828	100.0	1828	24	Human neuronal NAC
3	1828	100.0	1828	24	Human neuronal nic
4	557.6	30.5	1925	18	Neuronal nicotinic
5	555.8	30.4	1377	22	Human CHRN3 gene
6	554.2	30.3	1927	24	Human neuronal NAC
7	554.2	30.3	1927	24	Human neuronal nic
8	377.6	20.7	1638	22	Human CHRN3 parti

9	377.6	20.7	1638	22	AAD20870	Human CHRN3 parti
10	334.6	18.3	2277	15	AAV12199	Human neuronal nic
11	334.6	18.3	2277	16	AAQ90387	Alpha 2 subunit of
12	334.6	18.3	2277	24	ABV73243	Human neuronal NAC
13	334.6	18.3	2277	24	ABV73243	Human neuronal nic
14	334.6	18.3	2664	18	AAV48235	Neuronal nicotinic
15	334.6	18.3	2664	24	ABK92165	Prostate cancer-as
16	315.6	17.3	1908	18	AAV48236	Neuronal nicotinic
17	314.8	17.2	1743	18	AAV48232	Neuronal nicotinic
18	314.8	17.2	1743	24	ABV73247	Human neuronal NAC
19	314.8	17.2	1743	24	ABV73247	Human neuronal nic
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21	303.6	16.6	1654	24	ABV73244	Human neuronal NAC
22	303.6	16.6	1654	24	ABV73244	Human neuronal nic
23	303.6	16.6	1757	15	AAV12200	Human neuronal nic
24	303.2	16.6	1809	23	AAV12200	DNA encoding novel
25	303.2	16.6	2082	18	AAV59528	Alpha4 subunit of
26	303.2	16.6	3496	18	AAV48237	Neuronal nicotinic
27	296.2	16.2	299	24	ABL38070	Human colon tumour
28	294.4	16.1	1667	21	AAZ38821	Human acetylcholin
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31	290.4	15.9	2363	15	AAV12196	Human neuronal nic
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33	290.4	15.9	2363	24	ABV73245	Human neuronal nic
34	289.8	15.9	1350	14	AAQ35053	Alpha subunit of T
35	289	15.8	1350	14	AAQ39941	Acetylcholine rece
36	280.8	15.4	1869	24	AAV45873	Modified acetylcho
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39	269.2	14.7	1350	15	AAQ56918	Acetylcholine rece
40	261.4	14.3	1896	24	AAV45870	Modified acetylcho
41	261.4	14.3	1896	24	ABL54791	Modified hen ACR s
42	260	14.2	1869	24	AAV45864	Modified acetylcho
43	260	14.2	1869	24	ABL54788	Insect nicotinic A
44	244.8	13.4	2460	11	AAQ06086	Plasmid pZPC13 enc
45	239	13.1	1521	12	AAQ14288	Human neuronal nic

ALIGNMENTS

RESULT 1

AAV48238
ID AAT48238 standard; DNA; 1828 BP.

XX AAT48238;

AC AAT48238;

DT 09-APR-1997 (first entry)

DE Neuronal nicotinic acetylcholine receptor alpha-5 subunit DNA.

XX Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;

XX ligand-gated receptor; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 155..1561

XX FT /*tag= a

XX PN WO9641876-A1.

XX PD 27-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09775.

XX PR 07-JUN-1995; 95US-0484722.

XX PA (SIBI-) SIBIA NEUROSCIENCES INC.

XX PI Elliott KJ, Harpold MW;

XX

DR WPI; 1997-065463/06.
XX P-PSDB; AAW09024.
PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
PT used in screening to determine the effect of drugs on the receptor
XX Disclosure; Page 54-55; 108pp; English.
XX
XX A DNA sequence (AA748238) codes for the alpha-5 subunit (AAW09024) of
CC the human neuronal nicotinic acetylcholine receptor (nAChR). Host
CC cells, esp. mammalian cells or amphibian oocytes, carrying alpha-5
CC nucleic acids, opt. in combination with other alpha and/or beta
CC subunit nucleic acids (see also AA748232-37, AA748239-41), express
CC recombinant nAChR subunits useful for identifying cpds. that
CC modulate the activity of human nAChRs.
XX
XX Sequence 1828 BP; 496 A; 372 C; 419 G; 541 T; 0 other;
SQ

Query Match 100.0%; Score 1828; DB 18; Length 1828;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1828; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB |||||
61 CGACTCACACTCAGTGTCTGATCCCAAGATTCCGGTTCCCGCGCGCGGTTCGAGAG 120
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DB |||||
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1321 TAGAAACATTTGGAAGCTCGCTCAATTTCTATTTCGCTACATTACAAGACACATCATGAA 1380
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1980

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Qy 1321 TAGAAACACATTTGAGAGTGGCTCAATTTATTCGCTACATTAACAGACACATCATGAA 1380
Db 1321 TAGAAACACATTTGAGAGTGGCTCAATTTATTCGCTACATTAACAGACACATCATGAA 1380
Qy 1381 GGAATAATGATGTCGCTGAGGTTGTTGAAGATTTGAAATTCATAGCCAGGTTCTTGATCG 1440
Db 1381 GGAATAATGATGTCGCTGAGGTTGTTGAAGATTTGAAATTCATAGCCAGGTTCTTGATCG 1440
Qy 1441 GATGTTCTGAGACTTTTCTTTTCGTTTCAATTTGTTGAGTCTCTTGGCTTTTGTTC 1500
Db 1441 GATGTTCTGAGACTTTTCTTTTCGTTTCAATTTGTTGAGTCTCTTGGCTTTTGTTC 1500
Qy 1501 TGTATTATTAATGAGGCAATATATTAATACCAAGTTCATATTGGAATGCAATATAGTG 1560
Db 1501 TGTATTATTAATGAGGCAATATATTAATACCAAGTTCATATTGGAATGCAATATAGTG 1560
Qy 1561 AAGCTCCCAAGGAGTCAAGTATACATTTTAAACACATATATCTGATGACCTTA 1620
Db 1561 AAGCTCCCAAGGAGTCAAGTATACATTTTAAACACATATATCTGATGACCTTA 1620
Qy 1621 TAAATATTAAGAAATGTAAGTTATGTTAAATTTAGTCAAGCTTTTAAACAGACTAAGTT 1680
Db 1621 TAAATATTAAGAAATGTAAGTTATGTTAAATTTAGTCAAGCTTTTAAACAGACTAAGTT 1680
Qy 1681 GCTAACCTCAATTTATGTTAAACAGATGATCAATTTGAAACAGTGGCTGTATGACTGAAGT 1740
Db 1681 GCTAACCTCAATTTATGTTAAACAGATGATCAATTTGAAACAGTGGCTGTATGACTGAAGT 1740

Qy 1741 AATAACTGATGAGATACATTTGATCTTTGTAATAAATAGCAAAATATATCTGAAGT 1800
Db 1741 AATAACTGATGAGATACATTTGATCTTTGTAATAAATAGCAAAATATATCTGAAGT 1800
Qy 1801 AGTGAATAATCTAGTATTTGTTATCTCTGG 1828
Db 1801 AGTGAATAATCTAGTATTTGTTATCTCTGG 1828

RESULT 4
AAT48234

ID AAT48234 standard; DNA; 1925 BP.

XX AAT48234;

XX AC AAT48234;

XX DT 09-APR-1997 (first entry)

XX DE Neuronal nicotinic acetylcholine receptor beta-3 subunit DNA.

XX KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;

XX KM Ligand-gated receptor; ds.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FH CDS 98..1474

FT sig_peptide /*tag= a

FT mat_peptide /*tag= b

FT misc_feature /*tag= c

FT /*tag= d

FT /*note= "(Claim 52)"

XX WO9641876-A1.

XX PD 27-DEC-1996.

XX PF 07-JUN-1996; 96WO-US09775.

XX PR 07-JUN-1995; 95US-0484722.

XX PA (SIBI-) SIBIA NEUROSCIENCES INC.

XX PI Elliott KJ, Harpold MW;

XX WPI; 1997-065463/06.

XX P-PSDB; AAW09020.

XX Nucleic acids encoding nicotinic acetylcholine receptor sub-units -

XX used in screening to determine the effect of drugs on the receptor

XX Claim 14; Page 79-81; 108pp; English.

XX A DNA sequence (AAT48234) codes for the beta-3 subunit (AAW09020) of

XX the human neuronal nicotinic acetylcholine receptor (nAChR). It

XX was isolated from a human substantia nigra cDNA library using human

XX nAChR beta-3 subunit cDNA. Host cells, esp. mammalian cells or

XX amphibian oocytes, carrying beta-3 subunit nucleic acids,

XX optionally with alpha-2, alpha-3, alpha-4, alpha-5, alpha-6 and/or

XX alpha-7 nucleic acids (see also AAT48232, AAT48235-39), can be used to

XX express recombinant nAChR subunits for use in identifying cpds.

XX that modulate the activity of human nAChRs.

SQ Sequence 1925 BP; 508 A; 453 C; 422 G; 542 T; 0 other;

Query Match 30.5%; Score 557.6; DB 18; Length 1925;

Best Local Similarity 65.2%; Pred. No. 2.6e-125;

Matches 880; Conservative 0; Mismatches 419; Indels 51; Gaps 2;

Qy 278 TCTATTGCAAAACATGAAGATAGTTTGTCTTAAGGATTTATTTCAGACTACGAAGATGG 337

Query Match	30.4%	Score 555.8	DB 22	Length 1377
Best Local Similarity	66.2%	Pred. No. 6.2e-125		
Matches 859	Conservative 0	Mismatches 387	Indels 51	Gaps 2
QY	278	TCATTTGCCAAAACATGAAGATAGTTTTCCTTAAGGATTTATTTTCAAGACTACGAAAGATGG	337	
DB	70	TCAAATCGCGAAATGAAGATGCGCTCCTCAGACATTTGTTTCAAGGTTATTCAGAAATGG	129	
QY	338	GTTTCGTCTCTGTGGAAACACCTGAATGACAAAATAAAAAATAAAATTTGGACATGCAATATCT	397	
DB	130	GTCCGCCCTGTATTACATCTTANTGACACCATAAAGTATATTTTGGATTGAAATATCC	189	
QY	398	CAATTGGTGGATGTGGATGAGAAAATTCAGTTAATGACAAACAAACGTCCTGGTTGAAACAG	457	
DB	190	CAGCTTGTAGATGTGGATGAAAAGATCAGCTGATGACAAACCAATGTGTGGCTCAACAG	249	
QY	458	GAAATGATAGTGTAAATTTAAGATGMAACCTGTAGTACTATGGTGGAAATAAAGTTATA	517	
DB	250	GAAATGACACAGCACCAAGTTACCGTGGAAATCCCTGATGATTTATGGTGGGATCCCATTCAT	309	
QY	518	CGTGTTCCTTTACAGACTCTGTCTGGACACACAGACATCGTTTGTGTGATAATCAGAGTGA	577	
DB	310	AAAGTTCCATCAGAACTCTGTGGCTCTCTGACATAGTCTCTTTGAAATGCTGACGGC	369	
QY	578	CGTTTTGAAGGGACCAAGTACGAAAACAGTCATC---AGGTACAATGGCACTGCACTGG	634	
DB	370	CGCTTCGAAGGCTCCCTGTATGACCAAGGTCATCGTGAATCAAAACGGAACGTGTGCTGG	429	
QY	635	ACTCCACCGCAACCTACAAAAGTTCTGTACCATAGATGTGACGTTTTTCCCATTTGAC	694	
DB	430	ACCCCTCCCGCCAGCTACAAAAGCTCTGCACCATGGAACGTGCTTTTCCCGCTTCGAC	489	
QY	695	CTTCAGAACTGTTTCCATGAAATTTGGTTCTTGACATTATGATGGATCACAGGTTTGATATA	754	
DB	490	CGACAGAACTGCTCCATGAAGTTTGGATCTGACATTATGATGACCACTGGTTGACCTC	549	
QY	755	ATTCTAGAGGACCAAGATGTGAGCAAGAGAGATTTTTTTTGATAATGGAGAAATGGGAGATT	814	
DB	550	ATTTTGATCAATGAAATGTGACAGAGAAAAGACTTCTTCGTAAACGGAGAAATGGGAAATA	609	
QY	815	GTGAGTGCACAGGGAGCAAGAGAAACAGAACCGACAGCTGTTGCTGGTATCGTATGTC	874	
DB	610	CTGAATGCAAGGGGATGAGGGGAAACAGAAAGGACGGCGGTGTACTCTATCCCTTTATC	669	
QY	875	ACTTACTCATTTCTAATCAAGCGCCTGCCTCTCTTTTATACCTTGTTCCTTTATAATACCC	934	
DB	670	ACGTATTCCTTCGTCTGAGACGCTGCTTTTATCTATACCTCTTTCTCATCATCCCC	729	
QY	935	TGTAITGGGCTCTCATTTTTTAACTGTACTGTCTTCTATCTCTCTTCAAAATGAAGGTGAA	994	
DB	730	TGCTCGGGCTGTCTTTTCCCTAACAGTCTGTGTCTATTTTACCTTCGGATGAAGAGAA	789	
QY	995	AGAATTTGTCTCTGCACTTCAGTACTTGTGTCTTTGACTGTCTCTTCTCTGGTTATTGAA	1054	
DB	790	AAACTTTTCATTTCCACATCGGTCTTGGTTTCTCTGACAGTTTTTCTTTTAGTGATGAA	849	
QY	1055	GAGATCATACCATCTCTTCAAAAGTCATACCTTAATTCGGAGAGTATCTGGTATTATACC	1114	
DB	850	GAAATCATCCATCGTCTTCCAAAGTCATTCCTCTCATTCGGAGAGTACCTGCTGTTTCATC	909	
QY	1115	ATGATTTTTGTGACACTGTCAATATTATGGTAAACCGTCTTTCGCTATCAACATTCATCATCGT	1174	

XX The invention relates to a suitable host cell transfected with an
CC isolated nucleic acid molecule comprising a sequence of nucleotides or
CC ribonucleotides that encodes at least one alpha or beta subunit of a
CC human neuronal nicotinic acetylcholine receptor (NACHR). The compositions
CC and methods of the present invention, which provide a means to prepare
CC synthetic or recombinant receptors and receptor subunits that are
CC substantially free of contamination from many other receptor proteins,
CC are useful for observing the effect of a drug substance on a particular
CC subtype to perform in vitro screening of the drug substance in a test
CC system that is specific for humans. The antibodies can be used in
CC immunochemistry and for diagnostic and therapeutic applications. The
CC present sequence represents a human neuronal NACHR beta3 subunit
CC encoding cDNA.

Sequence 1927 BP: 508 A; 455 C; 422 G; 542 T; 0 other;

Query Match 30.3%; Score 554.2; DB 24; Length 1927;
Best Local Similarity 66.2%; Pred. No. 1.8e-124;
Matches 858; Conservative 0; Mismatches 388; Indels 51;

Qy	278	TCTATTCCAAAA	CATGGAAGATAGTTTGCCTTAAGGATTTATTTCAAGACTACGAAAGATGG	337
Db	167	TCAATGCCGAAAA	TGAAGATGCGCCTCCTCAGACATTTGTTTCCAAAGGTTATCAGAAATGG	226
Qy	338	GTTTCGTCTCTGGAACACCT	GAATGACAAATAAABAATAAAATTTTGACATTTGCAATATCT	397
Db	227	GTCGCGCCTGTATTCATCT	TAAATGACCAATAAAAGTATATTTTGGATTTGAAAATATCC	286
Qy	398	CAATTTGGTGGATGTGGATGAGAAAAAT	TCAGTTAATGACAAACAAACGCTCTCGTTTGGAAACAG	457
Db	287	CAGCTTGTAGATGTGGATGAAAAGAAAT	CAGCTGATGACAACCAATGTGTGGCTCAACACAG	346
Qy	458	GAATGGATAGATGTAAATTAAGATGGAACCT	CGATGACTATGGTGGAAATAAAGATTATA	517
Db	347	GAATGGACAGACCACAAAGTTAC	GTGGTGAATCTCTGATGATTATGGTGGGATCCATTCCATTT	406
Qy	518	CGTGTTCCTTCAGACTCTGTCTGACAC	CAGACATCTTTTGTGTGATAATGACAGATGGA	577
Db	407	AAAGTTCCATCAGAAATCTGTGTGGCTT	CCGTGACATAGTTCTCTTTGAAAATGCTGACGGC	466
Qy	578	CGTTTTCGAAGGGACCGACTAGCGAAAA	CAGTCAATC---AGGTACAAATGGCACTGTCACTCGG	634
Db	467	CGCTTCGAAGGCTCCCTGATGACCAAGT	CATCGTGAATCAAAACGGAACGTGTGTCTGG	526
Qy	635	ACTCCACGGGAAACTACAAAGTTCTGTAC	CAATAGATGTCAGTTTTTCCCATTTTGAC	694
Db	527	ACCCCTCCCGCAGCTACAAAAGCTCCTG	CACCAATGGACGTCACGTTTTTCCCGCTTCGAC	586
Qy	695	CTTCAGAACCTGTCCATGAAATTTGGTCT	CTTGGACATTATGATGATCACAGGTTGATATA	754
Db	587	CGACAGAACCTGCTCCATGGAAGTTTGG	ATCTCTGGAACCTATGATGCAACATGTTTGACCTC	646
Qy	755	ATTTCTAGAGACCAAGATGTAGACAA	CAGAGATTTTTTTTGATATGAGAAATGGGAGATT	814
Db	647	ATTTTGATCAATGNAATGTGACAGAAA	AGACTCTTCGATACGGGAATGGAATA	706
Qy	815	GTGAGTGCAACAGGAGCAAAAGGAAA	CAGAACCGACAGCTGTGTGCTGGTATCCGTATGTC	874
Db	707	CTGAATGCAAAAGGGGATGAAAGGGGAA	CAGAAAGGCGGTGTACTCCTATCCCTTTATC	766
Qy	875	ACTTACTCATTTGTAATCAAGCGCTCGCT	CTTTTATACCTTGTTCCCTTATAATATCCC	934
Db	767	ACGTATTTCTTCGTGCTGAGACGCTCGC	CTTATTCATACCCCTCTTCATCATATCCCC	826
Qy	935	TGTATTGGGCTCTCATTTTAACTGTACT	GTCTTCTATCTTCCTTCAAAATGAAGGTGAA	994
Db	827	TGCTGGGGCTGTCTTCCCTAAACAGT	CTCTTGTCTTATTACCTTCGGATGAAGHAA	886
Qy	995	AAGATTTGCTCTGCACTTCAGTACTTGTG	CTTTTGTACTGTCTTCCTTCCTTCCTTCGTTATTGAA	1054
Db	887	AAACCTTTATTCACATCCGCTCTTGTTT	CTCTGACAGTTTTTCTTTTAGTGAATGAA	946

PF 30-MAR-2001; 2001WO-US10277.
XX PR
XX 03-APR-2000; 2000US-194162P.
XX (GENA-) GENAISSANCE PHARM INC.
PA (CHEW/) CHEW A.
PA (CHOI/) CHOI J. Y.
PA (KOSH/) KOSHY B.
PA (STEP/) STEPHENS J. C.
XX PI
XX Chew A, Choi JY, Koshy B, Stephens JC;
XX WPI; 2001-626425/72.
XX
XX New polynucleotide, useful for studying expression and function of
PT CHRN3, comprises polymorphic variant of cholinergic receptor,
PT nicotinic, beta polypeptide 3 (CHRN3) gene, containing one of
PT polymorphic sites PS1-PS8 -
XX
XX Claim 19; Fig 5; 68pp; English.
XX
XX The invention relates to methods for haplotyping cholinergic receptor,
CC nicotinic, beta polypeptide 3 (CHRN3) gene. The invention also
CC provides single nucleotide polymorphisms (SNP) in the human CHRN3 gene.
CC Polymorphic variants of CHRN3 gene is used for screening for candidate
CC drugs to treat diseases related to CHRN3 activity. They are also useful
CC in studying the effect of variation on the biological activity of CHRN3
CC as well as on the binding affinity of candidate drugs targeting CHRN3
CC for treating Alzheimer's disease and other neurological disorders. They
CC are also useful in gene therapy. Compositions comprising CHRN3 gene
CC polymorphic variants are useful for genotyping and/or haplotyping a
CC CHRN3 gene in an individual. The present sequence is human CHRN3
CC partial gene. Human CHRN3 gene includes 8 polymorphic sites PS1-PS8.
XX
SQ Sequence 1638 BP; 480 A; 354 C; 363 G; 441 T; 0 other;

Query Match 20.7%; Score 377.6; DB 22; Length 1638;
Best Local Similarity 71.6%; Pred. No. 1.4e-81;
Matches 510; Conservative 0; Mismatches 199; Indels 3; Gaps 1;

QY 566 AATGAGATGGAGTTTGAAGGACGAGTACGAAACAGTCATC---AGGTACATGGC 622
DB |||||
QY 623 ACTGTACCTGGACTCCACCGCAAACTACAAAGTTCCTGTACCATAGATGTCACGTTT 682
DB |||||
QY 489 ACTGTGCTGGACCCCTCCCGCAGCTACAAAGTCTCCGACCATGGACGTCACGTTT 548
DB |||||
QY 683 TTCCCAATTTGACCTTCAGAACTGTTCATGAAATTTGGTTCTTGGACTTATGATGATCA 742
DB |||||
QY 549 TTCCCGTTCCAGCAGACAGACTGCTCCATGAAGTTTGGATCCTGGACTTATGATGGACC 608
DB |||||
QY 743 CAGGTTGATATAATTTCTAGAGGACCAAGATGTAGACAAAGAGATTTTTTTGATAATGGA 802
DB |||||
QY 609 ATGGTTGACCTCATTTTGTATCAATGAATGTGCACAGAAAGAACTTCTTCGATAACGGA 668
DB |||||
QY 803 GAATGGAGATGTGAGTGCACAGGGAGCAAGGAAACAGACCGACAGCTGTGCTGG 862
DB |||||
QY 669 GAATGGAAATGACTGAATGAAGGAGGATGAAGGGGACAGAGGGCGGTGACTCC 728
DB |||||
QY 863 TATCCGTTATGCTACTTACTTATGTAATCAAGCGCTGCTCTCTTTTATACCTTTTC 922
DB |||||
QY 729 TATCCCTTTATCAGTATTCCTTCGCTCGTAGAGCGCTGCTTTATTTCTATACCTCTTT 788
DB |||||
QY 923 CTTATAATACCTGTATGGGCTCTCATTTTTTAACCTGATCTGTCTTCTATCTCTCTCA 982
DB |||||
QY 789 CTATCATCCCTGCTGGGCTGCTCTTCTTAACAGTCTTGTGTCTTATTTACCTTCG 848
DB |||||
QY 983 AATCAGGTCAAGATTTGCTCTGACATCTCAGTACTTGTGCTTTGACTGTCTCTCTT 1042
DB |||||
QY 849 GATGAGGAGAGAAACATTTTATTCACATCGGCTTGGTTTCTCTGACAGTTTTCCTT 908
DB |||||
QY 1043 CTGTTATTGAAGAGATCATACCATCATCTTTCAAAAGTCATACCTCTTAATTGGAGAGTAT 1102
DB |||||

DB 909 TTAGTGATTGAAGAAATCATCCATCGTCTTCCAAAGTATTCTCTCTCATTTGGAGAGTAC 968
QY |||||
DB 1103 CTGGTATTTTACCATGATTTTGTGACACTGTCAATTATGTAACCGTCTTCGCTATCAAC 1162
DB |||||
DB 969 CTGCTGTTTATCATGATTTTGTGACCCCTGTCCATCATTTGTTACCGTGTGTTGTCATTAAC 1028
QY |||||
DB 1163 ATTATCATCTGTTCTTCTCAACACATAATGCCATGGCCCTTTGGTCGCGAAGATATTT 1222
DB |||||
DB 1029 GTTCACACAGATCTTCTTCCAGTACCACCCCATGGCCCTGGGTAAAGAGGCTCTTT 1088
QY |||||
DB 1223 CTTACACACGCTTCCAAACTGCTTTGCATGAGAGTCATGTAGACAGGTACT 1274
DB |||||
DB 1089 CTGCAGAAACTTCCAAATTTACTTTTGCATGAAGATCATGTGGATCGCTACT 1140

RESULT 9
AAD20870
ID AAD20870 standard; DNA; 1638 BP.
XX
AC AAD20870;
XX
DT 03-JAN-2002 (first entry)
XX
XX Human CHRN3 partial gene containing exon 5 #2.
XX
XX Human; cholinergic receptor, nicotinic, beta polypeptide 3; CHRN3;
KW single nucleotide polymorphism; SNP; drug screening; Alzheimer's disease;
KW neurological disorder; gene therapy; genotyping; haplotyping; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT misc_feature 253
FT /tag= a
FT /note= "This degenerate base represents polymorphic
FT site PS7"
FT misc_feature 268
FT /tag= b
FT /note= "This degenerate base represents polymorphic
FT site PS6"
XX
XX WO200175063-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US10277.
XX
XX 03-APR-2000; 2000US-194162P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX (CHEW/) CHEW A.
XX (CHOI/) CHOI J. Y.
XX (KOSH/) KOSHY B.
XX (STEP/) STEPHENS J. C.
XX
XX Chew A, Choi JY, Koshy B, Stephens JC;
XX WPI; 2001-626425/72.
XX
XX New polynucleotide, useful for studying expression and function of
PT CHRN3, comprises polymorphic variant of cholinergic receptor,
PT nicotinic, beta polypeptide 3 (CHRN3) gene, containing one of
PT polymorphic sites PS1-PS8 -
XX
XX Disclosure; Page 67; 68pp; English.
XX
XX The invention relates to methods for haplotyping cholinergic receptor,
CC nicotinic, beta polypeptide 3 (CHRN3) gene. The invention also
CC provides single nucleotide polymorphisms (SNP) in the human CHRN3 gene.
CC Polymorphic variants of CHRN3 gene is used for screening for candidate
CC drugs to treat diseases related to CHRN3 activity. They are also useful
CC in studying the effect of variation on the biological activity of CHRN3
CC as well as on the binding affinity of candidate drugs targeting CHRN3
CC for treating Alzheimer's disease and other neurological disorders. They
CC are also useful in gene therapy. Compositions comprising CHRN3 gene
CC polymorphic variants are useful for genotyping and/or haplotyping a
CC CHRN3 gene in an individual. The present sequence is human CHRN3
CC partial gene. Human CHRN3 gene includes 8 polymorphic sites PS1-PS8.
XX

CC as well as on the binding affinity of candidate drugs targeting CHRN3
CC for treating Alzheimer's disease and other neurological disorders. They
CC are also useful in gene therapy. Compositions comprising CHRN3 gene
CC polymorphic variants are useful for genotyping and/or haplotyping a
CC CHRN3 gene in an individual. The present sequence is human CHRN3
CC partial gene. Human CHRN3 gene includes 8 polymorphic sites PSI-P58.
XX
SQ Sequence 1638 BP; 480 A; 354 C; 362 G; 441 T; 1 other;

Query Match 20.7%; Score 377.6; DB 22; Length 1638;
Best Local Similarity 71.6%; Pred. No. 1.4e-81;
Matches 510; Conservative 0; Mismatches 199; Indels 3; Gaps 1;
QY 566 AATGAGATGACGTTTGAAGGACCAAGTACGAAACAGTCATC---AGGTACAATGGC 622
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 429 AGTGTGACGGCGCTTCCGAGGCTCCCTGATGACCAAGGTCATCGTGAATCAACCGA 488
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 623 ACTGTCACTGGACCTCCACCGCAACTACAAAGTCTCTGACCATAGATGTCACGTTT 682
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 489 ACTGTGTGTGACCCCTCCCGCCAGCTACAAAGCTCTCGACCATGAGCGTCACGTTT 548
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 683 TTCCCAATTTGACCTTCAGAACTGTTCCATGAATTTGGTCTTGGACTTATGATGATCA 742
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 549 TTCCCGTTCCGACGACAGACTGCTCCATGAAGTTTGGATCTGGACTTATGATGGCACC 608
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 743 CAGTTGTATATAATTTCTAGAGACCAAGATGTAGACAAGAGATTTTTTTGATAATGGA 802
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 609 ATGTTGTACCTCAATTTGATCAATGAAATGTGACAGAAAGACTTCTTCGATAACGGA 668
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 803 GAATGGAGATGTGAGTGCAACGGGAGCAAGAAAGCAAGACGACGCTGTGCTGG 862
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 669 GAATGGGAAATGACTGAATGCAAGGGGATGAAGGGGAAACAGAAAGGCGGTGTACTCC 728
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 863 TATCGTATGTCACTTACTTCTATTTGTAATCAAGCGCTGCCTCTCTTTTATACCTTGTTC 922
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 729 TATCCCTTATCAGTATTCCTCTGCTGAGACGCTGCCTTATTTCTATACCTCTTT 788
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 923 CTTATAATACCTGTATTGGCTCTCAATTTTAACTGTACTGTCTTCTATCTTCTTCA 982
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 789 CTCATCATCCCTGCTGCGGCTGCTCTTCTTAACAGTCTTGTGTTCTTATTTACCTTCG 848
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 983 AATGAGGTGAAAGATTTGCTCTGCACTTCAGTACTGTCTTTGACGTCTCTCTT 1042
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 849 GATGAAGGAGAAACATTTTCATATCCACATCGGCTTGGTTCTCTGACAGTTTCTCT 908
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1043 CTGTTTATGAAGAGATCATACCATCATCTTCAAAAGTCATACCTCTAATTTGGAGAT 1102
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 909 TTAGTGATTGAAGAAATCATCCATCGTCTTCCAAAGTCATCTCTCATTTGGAGATAC 968
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1103 CTGTTATTTACCATGATTTTGTGACACTGTCAATTTATGTAACCGTCTTCGCTATCAAC 1162
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 969 CTGCTGTTTCATCATGATTTTGTGACCTGTGTCATCATTTGTTACCGTGTGTTGTCATTAAC 1028
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1163 ATTCAATCATGTTCTTCTCAACATTAATGCCATGGCGCTTTGGTCCGCAAGATATT 1222
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1029 GTTCAACACAGATCTTCTTCCACGTACACCCCATGGCCCTGGTGTAAAGAGGCTCTTT 1088
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1223 CTTCAACAGCTTCCCAACTGCTTTGTCATGAGAGTTCATGTAGACAGTACT 1274
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1089 CTGAGAAACTTCCAAATTAATTTTGGATGAAGATCATGTGGATCGCTACT 1140
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
AAV12199 standard; cDNA; 2277 BP.
XX AAV12199
AC AAV12199;
XX 14-MAY-1998 (first entry)
XX Human neuronal acetylcholine receptor alpha-2 subunit cDNA.
XX Human neuronal nicotinic acetylcholine receptor; alpha-2 subunit;
KW Human; neuronal nicotinic acetylcholine receptor; alpha-2 subunit;

KW brain tissue; screening; NACHR; antibody; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
CDS 166..1755
FT /*tag= a
FT /product= "neuronal nicotinic acetylcholine receptor
FT alpha-2 subunit"
XX
XX WO9420617-A2.
XX 15-SEP-1994.
XX 08-MAR-1994; 94WO-US02447.
XX 08-MAR-1993; 93US-0028031.
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX (SIBI-) SIBIA NEUROSCIENCES INC.
XX Elliott KJ, Ellis SB, Harpold MW;
XX WPI; 1994-303024/37.
XX P-PSDB; AAW44155.
XX Human neuronal nicotinic acetylcholine receptor subunits and DNA -
XX also transformed cells useful for screening cpds. which modulate
XX activity of the receptor
XX Disclosure; Page 67-68; 99pp; English.

The present sequence encodes a human neuronal nicotinic acetylcholine
receptor (NACHR) subunit. The cells expressing the alpha and/or beta
NACHR subunits may be used in a method of screening compounds to
identify any which modulate the activity of human neuronal NACHR.
Subunit specific antibodies may be used to monitor the distribution
and expression density of various subunits in normal vs diseased brain
tissues. Testing of single receptor subunits or specific receptor
subunit combinations with a variety of potential agonists or antagonists
provides information with respect to the function and activity of the
individual subunits and should lead to the identification and design of
compounds that are capable of very specific interaction with one or
more receptor subtypes. The resulting drugs should exhibit fewer
unwanted side effects than drugs identified e.g. screening with cells
that express a variety of subtypes.

XX Sequence 2277 BP; 451 A; 695 C; 643 G; 486 T; 2 other;

Query Match 18.3%; Score 334.6; DB 15; Length 2277;
Best Local Similarity 61.3%; Pred. No. 4.7e-71;
Matches 595; Conservative 0; Mismatches 364; Indels 12; Gaps 3;

QY 292 TGAAGATAGTTTGTCTAAGGATTTATTTCAAGACTACGAAGATGGTTCGTCTGTGGA 351
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 339 TGAGGACCGGCTCTTCAACACACCTTTCGCGGGCTACACCGCTGGCGGCCCGGTGCC 398
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 352 ACACCTGAATGACAAAATAAATAAATTTGGACTTGCATATCTCAATTTGGTGGATGT 411
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 399 CAACACTTCAGACGTGGTGTGTTGGCGCTTTGGACTGTCCATCGCTCAGCTCATCGATGT 458
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 412 GGATGAGAAAAATCAGTTAATGACAAACAAACGCTCTGGTTCGAAACAGGAATGGATAGTGT 471
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 459 GGATGAGAGAACCAATGATGACCAACAGCTCTGGCTAAACAGAGGTGGACGACTA 518
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 472 AAAATTAAAGTGAACCCCTGATGATGTGGAATAAAGTTATACGTGTTCTTCTGGA 531
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 519 CAAACTCGCTGGAACCCCGCTGATTTTGGCAACATCACATCTCTCAGGGTCCCTTCTGA 578
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 532 CTCTGTCTGACACACCATCGTTTGTGTTGATGATGACAGATGGAGCTTTTGAAGGAC 591
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 579 GATGATCTGGATCCCGACATTTGTTCTTACTACAAACATGCGAGTGGGGAGTTTTCAGTGAC 638
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 592 ----CAGTACGAAACAGTCATCAGGTACATGACACTGTGACACTGTGACACTCCACCGGCAA 648
Db 639 CCATGATGACCAAGCCACCTCTTCCACGGGCACTGTGCACTGGGTGCGCCCGCCCAT 698
QY 649 CTACAAAAGTTCTGTACCATAGATGTGACGTTTTTCCCATTTGACCTTCAGAACTGTTTC 708
Db 699 CTACAAAGCTCTGTGACGATCGACGTGACCTTCTTCCCTTCGACGAGCAAGTGCAC 758
QY 709 CATGAAATTTGGTTCTTTGGACTTATGATGGATCACAGGTTGATATTAATTTAGAGGACCA 768
Db 759 GATGAAGTTTGGCTCTCGACTTATGACAAAGCCCAAGATCGACCTGGAGCAGATGGACA 818
QY 769 AGATGTAGACAGAGAGATTTTTTTGATATGAGAGATGGAGATGTGAGTGCACACAGG 828
Db 819 GACTGTGGACCTGAAGACTACTTGGAGAGCGGAGTGGGCCATCGTCAATGCCACGGG 878
QY 829 GAGCAAGGAAACAGAACCGACAGCTGTTGC-----TGGTATCCGTATGTCACTTACTC 882
Db 879 CACCTTAAACAGCAAGAGTACGACTGCTGCGCGGAGATCTACCCGAGCTCACCTACGC 938
QY 883 ATTTGTAATCAAGCGCTGCTCTCTTTTATACCTTGTTCCTTATATACCTGTATTGG 942
Db 939 CTTGTCATCCGGGGCTGCGCTCTTACACCATCACTCATCCCTGCGCTGCT 998
QY 943 GCTCTCAATTTTAACTGATCTGTCTTCTATCTTCTTCAATGAAAGTGAAAGATTGG 1002
Db 999 CATCTCTGCTCACTGTGCTGCTTCTTACCTGCGCTCGACTGCGGCGAGAGATCAC 1058
QY 1003 TCCTGCACCTTCACTGCTGCTTGTGCTTGTGCTTCTTCTTCTTCTTCTTCTTCTTCT 1062
Db 1059 GCTGTGATTTTGGTGTGCTGCTGCTTCACTCACCGTCTTCTGCTGCTCATCACTGAGATCAT 1118
QY 1063 ACCATCATCTTCAAAAGTCATACCTCTTAATTTGAGAGATGCTGGTATTTTACCATGATTTT 1122
Db 1119 CCGTCCACCTCGCTGGTCATCCGCTCATCCGGAGTACCTGCTTTCACCATGATCTT 1178
QY 1123 TGTGACACTGTCAATATGATGTAACCGTCTTCGCTATCAACATTCATCATGCTTCTTCTC 1182
Db 1179 CGTCACTCTGCTCATCGTATCACTCCGCTTTCGCTCAATGTGCAACACCGCTCCGCCAG 1238
QY 1183 AACACATATGCGATCGGCTTGTGCTGCGCAAGATATTTCTTCAACGCTTCCCAACT 1242
Db 1239 CACCCACA---CCATGCCCACTGGGTGCGGGGGGCCCTTCTGGGCTGTGTGCCCCGGTG 1295
QY 1243 GCTTTGCTATGA 1253
Db 1296 GCTTCTGATGA 1306

RESULT 11
AAQ90387
ID AAQ90387 standard; cDNA; 2277 BP.
XX AC AAQ90387;
XX DT 25-MAR-2003 (updated)
XX DT 30-NOV-1995 (first entry)
XX Alpha 2 subunit of a human neuronal nicotinic acetylcholine receptor.
DE Human nAChR; neuronal nicotinic acetylcholine receptor;
KW neurotransmitter; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
PH CDS 166..1755
FT /*tag= a
XX WO9513299-A1.
XX 18-MAY-1995.
XX

PF 08-NOV-1994; 94WO-US12859.
XX 08-NOV-1993; 93US-0149503.
XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
XX Elliott KJ, Ellis SB, Harpold WM;
XX WPI; 1995-194036/25.
DR P-PSDB; AAR73966.
XX New human neuronal nicotinic acetylcholine receptor alpha2 subunit DNA
PT used to develop prods. for detection, diagnosis and therapy and for
PT modulating activity
XX Claim 2; Page 43-46; 54pp; English.
PS DNA encoding the human nAChR alpha2 subunit was isolated from a
CC human thalamus tissue cDNA library using corresp. rat cDNA. The
CC insert of one clone obtd. was ligated with the insert of another
CC clone to generate a full-length alpha 2 subunit cDNA. The DNA can be
CC used to identify function nAChRs. Cells contg. the DNA can be used
CC for screening to identify cpds. which modulate the activity of human
CC nAChRs. The human nAChR alpha 2 subunit can be used to product
CC antibodies which can be used in immunohistochemistry, diagnosis and
CC therapy. The nucleic acids can be used for analysing disease states
CC and creating animal models.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 2277 BP; 451 A; 696 C; 643 G; 487 T; 0 other;
SQ Query Match 18.3%; Score 334.6; DB 16; Length 2277;
Best Local Similarity 61.3%; Pred. No. 4.7e-71;
Matches 595; Conservative 0; Mismatches 364; Indels 12; Gaps 3;
QY 292 TGAAGATGTTTGCCTTAAGGATTATTTCAAGACTAGCAAGATGGTTGCTCTGTGGA 351
Db 339 TGAGGACCGGCTCTTCAAAACACCTCTTCGGGGCTACAAACCGTGGCGCGCCCGGTGCC 398
QY 352 ACACCTGGAATGACAAAATAAAATTTGGACTTGAATATCTCAATTTGGTGGATGT 411
Db 399 CAACACTTCAGAGCTGGTGTATTTGGCTTTGGACTGTCCATCGCTCATCGATGT 458
QY 412 GGATGAGAAAATCAGTTAATGACAAACAGTCTGGTTGAAACAGGAATGGAATAGATGT 471
Db 459 GGATGAGAAAGAACAAATGATGACCAACAGTCTGGCTTAAACAGAGGTGGAGCGACTA 518
QY 472 AAAATTAGATGGAACCTGATGACTATGTTGGATATAAAGTTATACGTGTTCTTCAGA 531
Db 519 CAAACTGCGCTGGAACCCCGCTGATTTTGGCAACATCATCTCTCAGGGTCCCTTCTGA 578
QY 532 CTCTGTCTGGACACAGACATGTTTGTGATATGACAGATGGACGTTTGAAGGGAC 591
Db 579 GATGATCTGGATCCCGACATTTGTTCTTACACATGACAGATGGGAGTTGTCAGTGAC 638
QY 592 ---CAGTACGAAACAGTCAATCAGGTACAAATGGCACTGTGACCTGCACTCCACCGGCAA 648
Db 639 CCACATGACCAAGGCCACCTCTTCTCCACGGGCACTGTGCACTGGGTGCCCCCGCCAT 698
QY 649 CTACAAAAGTTCTGTACCATAGATGTGACGTTTTTCCCATTTGACCTTCAGAACTGTTTC 708
Db 699 CTACAAAGCTCTGTGACGATCGACGTGCTTCTTCCCTTCGACGAGCAAGTGCAC 758
QY 709 CATGAAATTTGGTTCTTTGGACTTATGATGGATCACAGGTTGATATTAATTTAGAGGACCA 768
Db 759 GATGAAGTTTGGCTCTCGACTTATGACAAAGCCCAAGATCGACCTGGAGCAGATGGACA 818
QY 769 AGATGTAGACAGAGAGATTTTTTTGATATGAGAGATGGAGATGTGAGTGCACACAGG 828
Db 819 GACTGTGGACCTGAAGACTACTTGGAGAGCGGAGTGGGCCATCGTCAATGCCACGGG 878
QY 829 GAGCAAGGAAACAGAACCGACAGCTGTTGC-----TGGTATCCGTATGTCACTTACTC 882

Db 1119 CCCTGACCTCGTGTGATCCCGCTCATCGCGAGTACCTGCTGTTCACCATGATCTT 1178
 Qy 1123 TGTGACACTGTCAATATATGTAACCGCTTCCTGCTATCAACATTCATCATGTTCTTCCTC 1182
 Db 1179 CGTACCTGCTCATGCTCATACCGCTTCCTGCTCAATGTGACACCGCTCCCGCAG 1238
 Qy 1183 AACACATAATGCCATGCGCGCTTTGGTCCGCAAGATATTTCTTTCACACGCTTCCCAAAC 1242
 Db 1239 CACCCACA---CCATGCCCACTGGGTGCGGGGGGCCCTTCTGGGCTGTGTGCCCCGGTG 1295
 Qy 1243 GCTTTGCATGA 1253
 Db 1296 GCTTCTGATGA 1306

RESULT 13

ABS54870
 ID ABS54870 standard; cDNA; 2277 BP.
 AC ABS54870;

XX 06-DEC-2002 (first entry)
 XX Human neuronal nicotinic acetylcholine receptor alpha 2 subunit cDNA.

DE Human neuronal nicotinic acetylcholine receptor; nNACHr; gene; ss;
 XX Human; neuronal nicotinic acetylcholine receptor; nNACHr; gene; ss;
 KW ion flux; alpha 2 subunit.
 KW Homo sapiens.

XX Key Location/Qualifiers
 FH 166..1755
 CDS /*tag= a
 FT /product= "Human nNACHr alpha 2 subunit"
 FT
 FT
 FT
 FT

XX US6440681-B1.

XX 27-AUG-2002.

XX 07-JUN-1995; 95US-0487596.
 XX 03-APR-1990; 90US-0504455.
 PR 30-NOV-1992; 92US-0938154.
 PR 08-MAR-1993; 93US-0028031.
 PR 08-NOV-1993; 93US-0149503.

XX (MERI) MERCK & CO INC.

XX Elliott KJ, Ellis SB, Harpold MM;
 WPI; 2002-711528/77.
 DR P-PSDB; ABG31800.

XX Identifying antagonists or agonists of human neuronal nicotinic
 FT acetylcholine receptors, by contacting recombinant cells with test
 PT compound, and measuring ion flux of cells or binding of compound to
 PT nNACHr -
 XX Claim 1; Column 29-32; 56pp; English.

XX The invention relates to a method for identifying compounds that are
 CC antagonists or agonists of human neuronal nicotinic acetylcholine
 CC receptors (nNACHrs), by contacting recombinant cells with a test
 CC compound and measuring ion flux, the electrophysiological response of the
 CC cells or binding of the test compound to the nNACHr. The recombinant
 CC cells are produced by transfection with a nucleic acid encoding at least
 CC one human nNACHr (alpha or beta) subunit, such that the cells express an
 CC nNACHr comprising one human subunit encoded by the transfected nucleic
 CC acid. This sequence represents cDNA encoding the alpha 2 subunit of the
 CC human nNACHr polypeptide.

XX Sequence 2277 BP; 451 A; 695 C; 643 G; 486 T; 2 other;

Query Match 18.3%; Score 334.6; DB 24; Length 2277;
 Best Local Similarity 61.3%; Pred. NO. 4.7e-71;
 Matches 595; Conservative 0; Mismatches 364; Indels 12; Gaps 3;
 Qy 292 TGAAGATAGTTGCTTAAGGATTTATTTCAAGACTACGAAGATGGTTGCTCTCTGGA 351
 Db 339 TGAGGACCGGCTCTTCAAAACACCTCTTCGGGGGTACAACCGCTGGGCGCGCCGCTGCC 398
 Qy 352 ACACTGATGACAAAATAAAATTTGGAGCTTGGCAATATCTCAATTTGGTGTGATGT 411
 Db 399 CAACACTTCAGAGCGGTGATTTGGCGCTTTGGAGCTGTCCATCGCTCAGCTCATCATGT 458
 Qy 412 GGATGAGAAAAATCAGTTAATGACAAACACCTCTGGTTGAAACAGGAATAGATAGATGT 471
 Db 459 GGATGAGAAAGAACCAAAATGATGACCAACACCTCTGGCTAAAAACAGGAGTGGAGCGACTA 518
 Qy 472 AAAATTAAGATGGNAACCTGATGACTATGTTGGATATAAAGTTATACGTGTTCTCTTCA 531
 Db 519 CAAACTGCGCTGGAACCCCGCTGATTTTGGCAACATCACATCTCTCAGGGTCCCTTCTGA 578
 Qy 532 CTCTGCTCGACACAGACATCGTTTGTGATATGAGATGAGACGTTTGAAGGGAC 591
 Db 579 GATGATCTGGATCCCGACATTTGTTCTTACAACATGAGATGGGAGTTTGCATGTAC 638
 Qy 592 ---CAGTACGAAAAACAGTATCAGGTACAAATGGCACTGTCACTGCACTCCACCGGCAAA 648
 Db 639 CCACATGACCAAGGCCACCTCTCTTCCACGGGCACTGTGCATCTGGGTGCCCGGCCCAT 698
 Qy 649 CTACAAAAGTTCTGTACCATAGATGACGTTTCCCTTTCCATTTGACCTTCAGAACCTGTC 708
 Db 699 CTACAAGAGCTCTGCGAGCATGACGTCACTTCTTCCCTTCGACCGAGAGAACTGCAA 758
 Qy 709 CATGAAATTTGTTCTTGGACTTATGATGGATCAGAGTTGATATATAATTTCTAGAGGACCA 768
 Db 759 GATGAAGTTTGGCTCTGAGCTTATGACAAGGCCAAGATCGACCTGGAGCAGATGAGCA 818
 Qy 769 AGATGTAGACAAGAGAGATTTTGTGATATGGAGATGGGAGATTTGTGAGTGCAACAGG 828
 Db 819 GACTGTGGACCTGAAGGACTACTTGGGAGAGCGCGAGTGGCCATCGTCAATGCCACGGG 878
 Qy 829 GAGCAAGGAACAGAACCGACGACTGTTGC-----TGGTATCCGTATGTCACTTACTC 882
 Db 879 CACCTACAACAGCAAGAAGTACGACTGTGCGCGAGAGATCTACCCCGAGCTCACCTACGC 938
 Qy 883 ATTTGTAATCAAGCGCTGCGCTCTCTTTTATACCTTGTTCCTTATATAACCTGTATTTG 942
 Db 939 CTTGCTATCCGGCGGCTGCGCTCTTCTACACCATCAACCTCATCATCCCTGCTGCT 998
 Qy 943 GCTCTCAATTTAACTGTACTTGTCTTCTATCTTCTTCAATGAAGGTGAAAGATTTG 1002
 Db 999 CATCTCTCGCTCACTGTGCTGTCTTCTTACCTGCGCTCCGACTGCGGCGAGAGATCAC 1058
 Qy 1003 TCTCTGCACTTCACTGTTGTCTTTGACTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1062
 Db 1059 GCTGTGCATTTCCGGTCTGCTGTCACTACCGCTTCTCTCTCTCTCTCTCTCTCTCTCT 1118
 Qy 1063 ACCATCATCTTCAAAAGTCACTACCTTAATTTGGAGAGTATCTGGTATTTTACCATGATTT 1122
 Db 1119 CCGTCCACTGCTGCTGCTATCCGCTCATCGCGAGTACCTGTCTGTTCACCATGATCTT 1178
 Qy 1123 TGTGACATGTCAATTTATGTAACCGCTTTCGCTATCAACATTCATCATCTGTTTCTCTC 1182
 Db 1179 CGTCACTCTGCTCATCGTCACTACCGCTTTCGCTCAATGTGCAACCGCTCCCGCAG 1238
 Qy 1183 AACACATAATGCGATGGCGCTTTGCTCGCAAGATATTTCTTTCACACGCTTCCCAAAC 1242
 Db 1239 CACCCACA---CCATGCCCACTGGGTGCGGGGGGCCCTTCTGGGCTGTGTGCCCGGTG 1295
 Qy 1243 GCTTTGCATGA 1253
 Db 1296 GCTTCTGATGA 1306

RESULT 14
 AAT48235
 ID AAT48235 standard; DNA; 2664 BP.
 XX
 AC AAT48235;
 DT 09-APR-1997 (first entry)
 XX
 DE Neuronal nicotinic acetylcholine receptor alpha-2 subunit DNA.
 XX
 KW Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
 KW ligand-gated receptor; dg.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 555..2141
 FT /*tag= a
 XX
 PN WO9641876-A1.
 XX
 PD 27-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US09775.
 XX
 PR 07-JUN-1995; 95US-0484722.
 XX
 PA (SIBI-) SIBIA NEUROSCIENCES INC.
 XX
 PI Elliott KJ, Harpold MM;
 XX
 DR WPI; 1997-065463/06.
 DR P-PSDB; AAW09021.
 XX
 PT Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
 PT used in screening to determine the effect of drugs on the receptor
 XX
 PS Disclosure; Page 49-52; 108pp; English.
 XX
 CC A DNA sequence (AAT48235) codes for the alpha-2 subunit (AAW09021) of
 CC the human neuronal nicotinic acetylcholine receptor (nAChR). Host
 CC cells, esp. mammalian cells or amphibian oocytes, carrying alpha-2
 CC nucleic acids, opt. in combination with other alpha and/or beta
 CC subunit nucleic acids (see also AAT48232-34, AAT48236-41), express
 CC recombinant nAChR subunits useful for identifying cpds. that
 CC modulate the activity of human nAChRs.
 XX
 SQ Sequence 2664 BP; 518 A; 815 C; 743 G; 588 T; 0 other;
 Query Match 18.3%; Score 334.6; DB 18; Length 2664;
 Best Local Similarity 61.3%; Pred. No. 5, 1e-71;
 Matches 595; Conservative 0; Mismatches 364; Indels 12; Gaps 3;
 QY 292 TGAAGATGTTGCTTAAGATTTATTCAGACTACGAAAGATGGTTCGTCTGTGGA 351
 DB 728 TGAGGACCGCTCTTCAACACCTCTTCGGGGCTACAACCGCTGGCGCGCGCGTGC 787
 QY 352 ACACCTGATGACAAATTAATAATTTGGACTTGCATATCTCAATTGGTGATGT 411
 DB 788 CAACACTTCAGACGGTGGTGAATTTGGCTTTGGACTGTCCATCGCTCAGCTCATCGATGT 847
 QY 412 GGATGAGAAATCAGTTAATGACAAACAAACCTCTGGTTGAAACAGGAATGGATAGTGT 471
 DB 848 GGATGAGAGAACCAATGATGACCAACCACTCTGGCTTAACAGGAGTGGAGCGACTA 907
 QY 472 AAAATTAAGATGAACCCCTGATGACTATGGTGAATAAAGTTATACGTTTCCTTCAGA 531
 DB 908 CAAACTGGCTGGAACCCCGCTGATTTGGCAACATCATCTCTCAGGTCCTCTCTGA 967
 QY 532 CTCTCTCTGGACACAGACATCGTTTGTGTAATGATGAGATGACGTTTGAAGGAC 591
 DB 968 GATGATCTGGATCCCGACATTTGTTCTCTACAAACATGAGATGGGAGTTTGCAGTGAC 1027

QY 592 ---CAGTACGAAACAGTCATCAGGTACAGTCAATGGCACTGTTCACCTGGACTCCACCGGCAAA 648
 DB 1028 CCACATGACCAAGCCACACCTCTTCTCCAGGGCACTGTGCACTGGTGGCCCGCCAT 1087
 QY 649 CTACAAAAGTTCTGTATACCATAGATGTCAGCTTTTCCCATTTGACCTTCAAGACTGTTC 708
 DB 1088 CTACAAGAGCTCTCTGCAGCATCGACGTCACCTTCTCCCTTCGACCGAGAACTGCAA 1147
 QY 709 CATGAAATTTGGTTCTTTGGACTTATGATGGATCACAGTTGATATAATTTCTAGAGGACCA 768
 DB 1148 GATGAAGTTTGGCTCTCTGGACTTATGACAAGGCCAAGATCGACCTGGAGCAGATGGAGCA 1207
 QY 769 AGATGTAGACAAGAGAGATTTTGTATAATGGAGAATGGAGAGTTGTGAGTGCACACAGG 828
 DB 1208 GACTGTGGACCTGAAGGACTACTGGGAGAGCGGAGTGGGCCATCGTCAATGCCACGG 1267
 QY 829 GAGCAAGAGAAACAGAACCCGACAGCTGTTC-----TGGTATCGGTATGTCACTTACTC 882
 DB 1268 CACCTACAACAGCAAGAGTACGACTGTGCGCGGAGATCTACCCCGACGTCACCTACGC 1327
 QY 883 ATTTGTAATCAAGCGCTCGCTCTCTTTTATACCTTGTTCCTTATAATACCTCTGATTGG 942
 DB 1328 CTTGCTCATCGGCGGCTGCGCTCTTCTACACCATCAACCTCATATCCCTCCCTGCTGCT 1387
 QY 943 GCTCTCAATTTTAACTGTACTTGTCTTCTATCTTCTTCTTCAAAATGAAGGTGAAAAGATTG 1002
 DB 1388 CATCTCGCTCACTGTGCTGGTCTTCTTACCTGCCCTCCGACTCGCGGAGAGATCAC 1447
 QY 1003 TCTCTGCACTTCACTGTGTCTTTGACTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1062
 DB 1448 GCTGTGCAATTCGGTGTGTGTCTCACTCAGCGTCTTCTGCTGTCTCATCTGAGATCAT 1507
 QY 1063 ACCATCATCTTCAAAAGTCATACCTCTAATTTGGAGAGTATCTGTTATTTACCATGATTTT 1122
 DB 1508 CCGTTCACCTCGCTGTGTCTATCCGCTCATCGGAGTACTGCTGTCTTCTCACCATGATCTT 1567
 QY 1123 TGTGACACTGTCAATTTATGTTAAACCGCTCTTCCGCTTATCAACATTCATCATGTTCTTCTC 1182
 DB 1568 CGTCACCTGTCCATCGTCATCACCGTCTTCTGCTCAATGTGCACACCGCTCCCGCAG 1627
 QY 1183 AACACATAATGCGATGCGGCTTTGGTCCGCAAGATATTTCTTTCACACGGTTCCTCAAACT 1242
 DB 1628 CACCCACA---CCATGCCCACTGGGTGGCGGGGGCCCTTCTGGGCTGTGTGCCCCCGGTG 1684
 QY 1243 GCTTTGCAATGA 1253
 DB 1685 GCTTCTGATGA 1695
 RESULT 15
 ABK92165
 ID ABK92165 standard; DNA; 2664 BP.
 XX
 AC ABK92165;
 XX
 DT 15-AUG-2002 (first entry)
 XX
 DE Prostate cancer-associated DNA sequence #51.
 XX
 KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
 KW gene therapy; gene; ds.
 XX
 OS Mammalia.
 XX
 PN WO20020268-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US32045.
 XX
 PR 13-OCT-2000; 2000US-0687576.
 PR 08-DEC-2000; 2000US-0733288.

PR 08-DEC-2000; 2000US-0733742.
PR 24-JAN-2001; 2001US-263957P.
PR 16-MAR-2001; 2001US-276791P.
PR 16-MAR-2001; 2001US-276888P.
PR 06-APR-2001; 2001US-281922P.
PR 24-APR-2001; 2001US-286214P.
PR 30-APR-2001; 2001US-0847046.
PR 04-MAY-2001; 2001US-288589P.
XX (BOSB-) EOS BIOTECHNOLOGY INC.
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX WPI; 2002-471335/50.
XX P-PSDB; ABG61850.
XX Detecting a prostate cancer-associated transcript in a cell in a
XX patient, useful for diagnosing prostate cancer (PC) or screening
XX modulators of PC, by determining if prostate cancer-associated genes
XX are expressed in a prostate tissue -
XX Claim 22; Page 338; 436pp; English.
XX The present invention relates to methods of detecting a prostate
XX cancer-associated transcript in a cell from a patient. The method
XX comprises contacting a biological sample from the patient with
XX prostate cancer-associated polynucleotides (designated PC genes) that
XX selectively hybridize to a sequence that is at least 80% identical
XX to them. The prostate cancer-associated polynucleotide sequences
XX are differentially expressed in prostate tumour tissue or in
XX prostate cancer and are derived from the tissues of various
XX organisms such as humans or other mammals (e.g. mice, sheep and dogs).
XX The methods of the invention are useful for diagnosing and treating
XX prostate cancer in mammals. The prostate cancer-associated genes are
XX useful for diagnosing or treating prostate cancer, as well as for
XX identifying modulators of prostate cancer or agents that inhibit
XX prostate cancer. The nucleic acid sequences are particularly useful
XX in gene therapy, as a vaccine or in antisense applications.
XX ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
XX sequences.
XX Sequence 2664 BP; 518 A; 815 C; 743 G; 588 T; 0 other;
SQ

Query Match 18.3%; Score 334.6; DB 24; Length 2664;
Best Local Similarity 61.3%; Pred. No. 51e-71;
Matches 595; Conservative 0; Mismatches 364; Indels 12; Gaps 3;
QY 292 TGAAGATAGTTTGGTTAAGGATTATTTCAAGACTACGAAAGATGGGTTCTGCTGTGGA 351
DB 728 TGAGGACCGGCTCTTCAACACCTCTTCGGGGCTACACCGCTGGGGCGCGCGGTGC 787
QY 352 ACACCTGAATGACAAATAAATAATTTGGACTTGGCAATATCTCAATTTGGTGGATGT 411
DB 788 CAACACTTCAGACGTTGGTGGTATTTGGCGCTTTGGACTGTCCATCGCTCATCGATGT 847
QY 412 GGATGAGAAAATCAGTTAATGACAAACACGCTGCTGTGTAACACGAGATGGATAGATGT 471
DB 848 GGATGAGAGAACCAATGATGACCAACAGCTGGCTTAACACAGGAGTGGAGCGACTA 907
QY 472 AAAATTAAAGATGGAACCCCTGATGACTATGGTGGAAATAAAGTTATACGTTTCTTTCAGA 531
DB 908 CAAACTCGCTGGAACCCCGCTGATTTTGGCAACATCACATCTCTCAGGGTCCCTTCTGA 967
QY 532 CTCTGTCTGACACCAACATCGTTTGTGTTGTAATGAGAGATGGAGCTTTTGAAGGGAC 591
DB 968 GATGATCTGGATCCCGACATCTTCTCTACCAACATGAGATGGGGAGTTTGCAGTGC 1027
QY 592 ---CAGTACGAAACAGTCACTAGGTACATGAGTGGCACTGACCTGGAGCTCCACCGGCAAA 648
DB 1028 CCACATGACCAAGGCCACCTCTTCTCAGGGGACATGTGACATGGGTGCCCGGCCAT 1087
QY 649 CTACAAAGTTTCTGTACCATAGATGTACGTTTTCCTCCATTTGACCTTCAGAACTGTTTC 708

DB 1088 CTACAAGAGCTCCTGCGAGCATCGAGCTCACCTTCTTCCCTTCGACCCAGCAGAACTGCAC 1147
QY 709 CATGAAATTTGGTTCTTGGACTTATGATGGATCACAGGTTGATATAATTTCTAGAGGACCA 768
DB 1148 GATGAAATTTGGTTCTTGGACTTATGACAAAGCCAGATCGACCTGGAGCAGATGAGCA 1207
QY 769 AGATGTAGACAAGAGAGATTTTGTGATTAATGGAGAAATGGGAGATTTGTGAGTGCACAGG 828
DB 1208 GACTGTGGACCTGAAGGACTACTTGGGAGAGCGCGAGTGGGCCATCGTCAATGCCACGGG 1267
QY 829 GAGCAAGGAAACAGAACCGACAGCTGTTGC-----TGGTATCCGTATGCTCACTTACTC 882
DB 1268 CACCTACAACAGCAAGAGTACGACTGTGCGCGGAGATCTACCCCGAGCTCACCTACGC 1327
QY 883 ATTTGTAATCAAGCGCTGCTCTCTTTTATACCTTGTTCCTTATAATACCCCTGTATTTGG 942
DB 1328 CTTGTGATTCGGCGGCTGCGCTCTTCTACCATCAACCTCATCATCTCCCTGCTGCT 1387
QY 943 GCTCTCATTTTAACTGTACTTGTCTTCTTATCTTCTTCAAAATGAAGGTGAAGAAATTTG 1002
DB 1388 CATCTCTGCTCACTGTGCTGTCTTCTTCTTCTTCTGCTCCGCTCCGACTGCGGCGAGAATCAC 1447
QY 1003 TCTCTGCACTTCAGTACTTGTGTCTTTGACTGTCTTCTTCTTCTTCTTCTTCTTCTTCTC 1062
DB 1448 GCTGTGCAATTCGGTGTGCTGTCTCACTCACCGCTTCTTCTGCTGCTCATCATCATGAGATCAT 1507
QY 1063 ACCATCATCTTCAAAAGTCACTACCTTAATTTGGAGAGTATCTGGTATTTTACCATGATTTT 1122
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QY 1243 GCTTTGCATGA 1253
DB 1685 GCTTCTGATGA 1695

Search completed: December 23, 2003, 18:47:17
Job time : 537 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: December 23, 2003, 15:35:43 ; Search time 6774 Seconds
(without alignments)
11039.681 Million cell updates/sec

Title: US-09-703-951A-7
Perfect score: 1828
Sequence: 1 CCCGCGGAGCTGTGGCGC.....ATCTAGTATTGTATCTCTGG 1828

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
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- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
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- 38: em.sy.*
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- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	1828	100.0	1828	6	AR282831	AR282831 Sequence
3	1828	100.0	1828	6	AX658380	AX658380 Sequence
4	1828	100.0	1828	6	AX719084	AX719084 Sequence
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6	1821.6	99.6	2468	9	BC033639	BC033639 Homo sapi
7	1642.6	89.9	1662	9	AF385586	AF385586 Homo sapi
8	1628.6	89.1	1679	9	HSMANICRC	MB3712 H. sapiens n
9	1405.4	76.9	1407	9	HSMACHRA5	Y08419 H. sapiens m
10	1212.2	66.3	1645	4	AF487464	AF487464 Bos tauru
11	1022.2	55.9	2895	10	RATNACHRR	J05231 Rat neurona
12	968.2	53.0	1445	10	AF204689	AF204689 Mus muscu
13	897.4	49.1	1365	5	CHKA5SUBU	J05642 Gallus dome
14	839.8	45.9	1526	9	HSK306485	AJ306485 Homo sapi
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19	597.2	32.7	238816	2	AC108616	AC108616 Rattus no
20	587.8	32.2	185429	2	AC122777	AC122777 Mus muscu
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39	376	20.6	44285	2	AC103843	AC103843 Homo sapi
40	376	20.6	150647	2	AF311104	AF311104 Homo sapi
41	376	20.6	154179	9	AC087533	AC087533 Homo sapi
42	363.2	19.9	176961	5	AL928917	AL928917 Zebrafish
43	353	19.3	245121	2	AC126482	AC126482 Rattus no
44	351.6	19.2	221259	2	AC102544	AC102544 Mus muscu
45	346.8	19.0	71864	2	AC103852	AC103852 Homo sapi

ALIGNMENTS

RESULT 1
AR224028
LOCUS AR224028 1828 bp mRNA linear PAT 26-SEP-2002
DEFINITION Sequence 7 from patent US 6440681.
ACCESSION AR224028
VERSION AR224028.1 GI:23332636
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE
1 (bases 1 to 1828)
Elliott,K.J., Ellis,S.B. and Harpold,M.M.
AUTHORS Methods for identifying agonists and antagonists for human neuronal
TITLE nicotinic acetylcholine receptors
JOURNAL Patent: US 6440681-A 7 27-AUG-2002;

AUTHORS Elliott, K.J. and Harpold, M.M.
TITLE Human neuronal nicotinic acetylcholine receptor compositions and methods employing same
JOURNAL Patent: US 6524789-A 7 25- Feb-2003;
FEATURES Location/Qualifiers
source 1..1828
BASE COUNT 496 a 372 c 419 g 541 t
ORIGIN /organism="unknown"

Query Match 100.0%; Score 1828; DB 6; Length 1828;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1828; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION	M83712	
ACCESSION	M83712.1	GI:177925
VERSION		
KEYWORDS	nicotinic receptor alpha 5 subunit.	
SOURCE	Homo sapiens	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE	1 (bases 1 to 1679)	
NICOTINIC	Chini, B., Clementi, P., Hukovic, N. and Sher, E.	
RECEIVED	5-nicotinic receptor subunit gene are expressed in neuronal and nonneuronal human cell lines	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 89 (5): 1572-1576 (1992)	

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Db 1679 A 1679

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LOCUS H. sapiens mRNA for nicotinic acetylcholine receptor alpha5 subunit
DEFINITION precursor.
ACCESSION Y08419
VERSION Y08419.1 GI:1702913
KEYWORDS nAChR gene; nicotinic acetylcholine receptor alpha 5 subunit.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Groot Kormelink, P.J. and Luyten, W.H.
TITLE Cloning and sequence of full-length cDNAs encoding the human
neural nicotinic acetylcholine receptor (nAChR) subunits beta3
and beta4 and expression of seven nAChR subunits in the human
neuroblastoma cell line SH-SY5Y and/or IMR-32
JOURNAL FEBS Lett. 400 (3), 309-314 (1997)
MEDLINE 97162233
PUBMED 9009220
REFERENCE 2 (bases 1 to 1407)
AUTHORS Groot Kormelink, P.J.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-1996) P.J. Groot Kormelink, Janssen Research
Foundation, Exp. Mol. Biol. Dept., Turnhoutseweg 30, B-2340 Beerse,
BELGIUM

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Qy 215 GCGGGCGCTGCGGTCTAGCGGGCGCGGGCGCGCGAGAGGANTATCTGAACCT 274
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RESULT 10
LOCUS AF487464
DEFINITION Bos taurus neuronal nicotinic acetylcholine receptor alpha5 subunit
mRNA, complete cds.
ACCESSION AF487464
VERSION AF487464.1 GI:19423863
KEYWORDS Bos taurus (cow)
SOURCE Bos taurus
ORGANISM Bos taurus
REFERENCE 1 (bases 1 to 1645)
AUTHORS Campos-Caro, A., Smillie, F. I., Dominguez del Toro, E., Rovira, J. C.,
Vicente-Agullo, F., Chapuli, J., Juiz, J. M., Sala, S., Sala, F.,
Ballesta, J. J., and Criado, M.
TITLE Neuronal nicotinic acetylcholine receptors on bovine chromaffin
cells: cloning, expression, and genomic organization of receptor
subunits
J. Neurochem. 68 (2), 488-497 (1997)
JOURNAL 97156643
MEDLINE 9003033
PUBMED 9003033
REFERENCE 2 (bases 1 to 1645)
AUTHORS Campos-Caro, A. and Criado, M.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2002) Bioquímica y Biología Molecular, Instituto
de Neurociencias, CSIC-UMH, Ctra. Valencia-Alicante Km 87, San
Juan, Alicante 03550, Spain
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RESULT 12

AF204689

LOCUS

AF204689 1445 bp mRNA linear ROD 22-DEC-1999

DEFINITION Mus musculus nicotinic acetylcholine receptor alpha 5 subunit
(Acras5) mRNA, partial cds.
ACCESSION AF204689
VERSION AF204689.1 GI:6625910
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1445)
AUTHORS Stitzel, J.A. and Blanchette, J.M.
TITLE Cloning of mouse nicotinic receptor alpha 5 subunit cDNA
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1445)
AUTHORS Stitzel, J.A. and Blanchette, J.M.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-1999) Pharmacology, University of Michigan, 1500
E. Medical Center Drive CCGC 2150, Ann Arbor, MI 48109-0930, USA
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RESULT 13
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Gallus domesticus nicotinic acetylcholine receptor alpha-5 subunit
gene, complete cds.

ACCESSION

J05642

VERSION

J05642.1

KEYWORDS

Gallus gallus (chicken)

SOURCE

Gallus gallus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 1365)

AUTHORS

Couturier,S., Erkman,L., Valera,S., Rungger,D., Bertrand,S.,
Boulter,J., Ballivet,M. and Bertrand,D.

TITLE

Alpha 5, alpha 3, and non-alpha 3. Three clustered avian genes
encoding neuronal nicotinic acetylcholine receptor-related subunits

JOURNAL

J. Biol. Chem. 265 (29), 17560-17567 (1990)

MEDLINE

91009210

PUBMED

1698777

COMMENT

Original source text: Chicken cDNA to mRNA and DNA.

FEATURES

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372..1203

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Qy	1031	ACTGTCTTCTTCTGTTTATGAAGAGATCATACCATCATCTTCAAAAGTCATACCTCTA	1090		
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Qy	1151	TTGCTATCAACATTCATCATCGTTCTTCTCAACACATATATGCGATGCGGCTTTGTC	1210		
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Qy	1211	CGCAAGATATTTCTTACACGCTTCCCAAACTGCTTTCATGAGAGTCATGTAGACAGG	1270		
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Qy	1331	TTGAAGTGGCTCAATTTCTATTCGCTTACATTAACAGACATCATGAAGAAATGAT	1390		
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BC050469/c
LOCUS BC050469
DEFINITION Homo sapiens, clone IMAGE:6189913, mRNA.
ACCESSION BC050469

BC050469.1	GI:29791534				
VERSION	Homo sapiens (human)				
KEYWORDS	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
SOURCE	1 (bases 1 to 2194)				
ORGANISM	Strausberg, R.				
REFERENCE	Submitted (08-APR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
AUTHORS	NIH-MGC Project URL: http://mgc.nci.nih.gov				
TITLE	Contact: MGC help desk				
JOURNAL	Email: cgapbs-remail.nih.gov				
REMARK	Tissue Procurement: Dr. James R. Lupski				
COMMENT	cDNA Library Preparation: Life Technologies, Inc.				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
	DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305				
	Web site: http://www-shgc.stanford.edu				
	Contact: (Dickson, Mark) mcd@paxil.stanford.edu				
	Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.				
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov				
	Series: IRAK Plate: 98 Row: 1 Column: 5				
	This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.				
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	/tissue_type="Peripheral Nervous System, sympathetic trunk"				
	/clone_lib="Lupski_sympathetic_trunk"				
	/lab_host="DH10B"				
	/note="vector: pCMV-SPORT6"				
BASE COUNT	744 a	460 c	390 g	600 t	
ORIGIN					
Query Match	45.9%; Score 838.2; DB 9; Length 2194;				
Best Local Similarity	98.5%; Pred. No. 4e-169;				
Matches	846; Conservative 0; Mismatches 13; Indels 0; Gaps 0;				
Qy	551	ATCGTTTGTGTTGATGATGAGTGGACGTTTGAAGGACGACGATGACGATC	610		
Db	1489	ATATGTGTGTTATTTAGTGCAGATGGAGTTTGAAGGACGACGATGACGATC	1430		
Qy	611	AGGTACATGCACTGTCACCTGGACTCCACGGCAAACTCAAAAGTTCCTGTACCAT	670		
Db	1429	AGGTACATGCACTGTCACCTGGACTCCACGGCAAACTCAAAAGTTCCTGTACCAT	1370		
Qy	671	GATGTGACGTTTTCCTTCCATTTGACCTTCAGAACTGTTCATGAAATTTGGTTCCTGGACT	730		
Db	1369	GATGTGACGTTTTCCTTCCATTTGACCTTCAGAACTGTTCATGAAATTTGGTTCCTGGACT	1310		
Qy	731	TATGATGATCAGAGTTGATATATTTCTAGAGGACCAAGATGTAGACAGAGATTTT	790		
Db	1309	TATGATGATCAGAGTTGATATATTTCTAGAGGACCAAGATGTAGACAGAGATTTT	1250		
Qy	791	TTTGATAATGAGATGGAGATTTGTGAGTGCACAGGAGCAAGGAAACAGAACCGAC	850		
Db	1249	TTTGATAATGAGATGGAGATTTGTGAGTGCACAGGAGCAAGGAAACAGAACCGAC	1190		
Qy	851	AGCTGTCTGCTGATCCGTATGTCACCTTACTTACTTATTAATCAAGCGCTGCTCTCTTT	910		
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Qy 911 TATACCTTGTTCCTTATAATACCTGTATTGGGCTCTCATTTTAACTGTACTGTCTTC 970
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Creation date: 02-19-2004
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